

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 10:27:11 ; Search time 21 Seconds
(without alignments)
27.483 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31

Sequence: 1 VQRGGR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 31 | 100.0 | 114 | 2 C35720 | hypothetical 12.4K |
| 2 | 31 | 100.0 | 351 | 2 AB2963 | endoglucanase [imp |
| 3 | 31 | 100.0 | 351 | 2 C98320 | hypothetical prote |
| 4 | 31 | 100.0 | 394 | 2 I39712 | endoglucanase - Ag |
| 5 | 31 | 100.0 | 567 | 2 T43555 | Ras pathway intera |
| 6 | 31 | 100.0 | 1151 | 2 A45226 | integrin alpha-1 c |
| 7 | 30 | 96.8 | 269 | 2 T31318 | hypothetical prote |
| 8 | 30 | 96.8 | 1131 | 2 T09701 | phytochrome - Scot |
| 9 | 28 | 90.3 | 134 | 2 B69156 | hypothetical prote |
| 10 | 28 | 90.3 | 235 | 2 S39652 | secretion protein |
| 11 | 28 | 90.3 | 245 | 2 B33422 | probable short-cha |
| 12 | 28 | 90.3 | 281 | 1 D30191 | conserved hypochet |
| 13 | 28 | 90.3 | 283 | 2 A13199 | B. subtilis YviA (|
| 14 | 28 | 90.3 | 283 | 2 AD1764 | B. subtilis YviA (|
| 15 | 28 | 90.3 | 325 | 1 A48561 | inner capsid prote |
| 16 | 28 | 90.3 | 328 | 1 VPXRC3 | minor inner core p |
| 17 | 28 | 90.3 | 338 | 2 D83349 | hypothetical prote |
| 18 | 28 | 90.3 | 375 | 1 K2BEF3 | thymidine kinase (|
| 19 | 28 | 90.3 | 393 | 2 B97128 | probable flavoprot |
| 20 | 28 | 90.3 | 449 | 2 B82958 | probable transport |
| 21 | 28 | 90.3 | 481 | 2 T28900 | hypothetical prote |
| 22 | 28 | 90.3 | 502 | 2 G87433 | conserved hypochet |
| 23 | 28 | 90.3 | 509 | 2 D69832 | probable Rieske [2 |
| 24 | 28 | 90.3 | 526 | 2 T20086 | hypothetical prote |
| 25 | 28 | 90.3 | 537 | 2 A33572 | oligopeptide-bind |
| 26 | 28 | 90.3 | 551 | 1 HQDVUG | cytochrome-c3 hydr |
| 27 | 28 | 90.3 | 577 | 2 E72396 | ABC transporter, A |
| 28 | 28 | 90.3 | 877 | 2 T03098 | p37 protein - Toxo |
| 29 | 28 | 90.3 | 881 | 1 VCLJG3 | env polyprotein - |

ALIGNMENTS

RESULT 1

C35720
hypothetical 12.4K protein - Escherichia coli
N;Alternate names: hypothetical protein 114
C;Species: Escherichia coli
C;Date: 05-Oct-1990 #sequence_revision 19-Mar-1993 #text_change 08-Oct-1999
C;Accession: C35720
R;Chen, C.M.; Ye, Q.Z.; Zhu, Z.; Wanner, B.L.; Walsh, C.T.
J. Biol. Chem. 265, 4461-4471, 1990
A;Title: Molecular biology of carbon-phosphorus bond cleavage. Cloning and sequencing of
A;Reference number: A35718; MUID:90170953; PMID:2155230
A;Accession: C35720
A;Molecule type: DNA
A;Residues: 1-114 <CHE>
A;Cross-references: GB:J05260; NID:gl47192; PIDN:AAA24351.1; PID:g455183
C;Genetics:
A;Start codon: GTG
C;Superfamily: Escherichia coli hypothetical 12.4K protein

Query Match 100.0%; Score 31; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 VQRGGR 6

Db

40 VQRGGR 45

RESULT 2

AB2963
endoglucanase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AB2963
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
star, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608950; PMID:11743193
A;Accession: AB2963
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-351 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44120.1; PID:gi7741690; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: celC
A;Map position: linear chromosome

A;Map position: linear chromosome

Query Match 100.0%; Score 31; DB 2; Length 351;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
 |||||
 Db 157 VQGGGR 162

RESULT 3

C98320
 hypothetical protein AGR_L3023GL [imported] - Agrobacterium tumefaciens (strain C58, Ce
 C;Species: Agrobacterium tumefaciens
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C;Accession: C98320
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markez, B.;
 Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: C98320
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-351 <KUR>
 A;Cross-references: GB:AE007870; PIDN:AAK90085.1; PID:g15160071; GSPDB:GN00170
 C;Genetics:
 A;Gene: AGR_L3023gl
 A;Map position: linear chromosome

Query Match 100.0%; Score 31; DB 2; Length 351;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
 |||||
 Db 157 VQGGGR 162

RESULT 4

I39712
 endoglucanase - Agrobacterium tumefaciens
 C;Species: Agrobacterium tumefaciens
 C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 08-Oct-1999
 C;Accession: I39712
 R;Matthysse, A.G.; White, S.; Lightfoot, R.
 J. Bacteriol. 177, 1069-1075, 1995
 A;Title: Genes required for cellulose synthesis in Agrobacterium tumefaciens.
 A;Reference number: I39709; MUID:95184586; PMID:7860385
 A;Accession: I39712
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-394 <RES>
 A;Cross-references: GB:L38609; NID:g710486; PIDN:AAC41433.1; PID:g710490
 C;Genetics:
 A;Gene: celC

Query Match 100.0%; Score 31; DB 2; Length 394;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
 |||||
 Db 262 VQGGGR 267

RESULT 5

T43555
 Ras pathway interacting protein Moel - fission yeast (Schizosaccharomyces pombe)
 N;Alternate names: elongation initiation factor subunit [misidentification]; Scd1 bindin
 C;Species: Schizosaccharomyces pombe
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 17-Mar-2000
 C;Accession: T43555; T38999
 R;Chen, C.R.; Li, Y.C.; Chen, J.; Hou, M.C.; Papadaki, P.; Chang, E.C.

Proc. Natl. Acad. Sci. U.S.A. 96, 517-522, 1999
 A;Title: Moel, a conserved protein in Schizosaccharomyces pombe, interacts with a Ras ef
 A;Reference number: 222574; MUID:99110922; PMID:9892665
 A;Accession: T43555
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-567 <CHE>
 A;Cross-references: EMBL:AF038568; NID:g4176720; PIDN:AA008893.1; PID:g4176721
 R;Purnelle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, December 1998

A;Reference number: 221823
 A;Accession: T38999
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-366; E, 368-567 <PUR>
 A;Cross-references: EMBL:AL034583; PIDN:CAA22586.1; GSPDB:GN00066; SPDB:SPAC637.07
 A;Experimental source: strain 972h-; cosmid c637
 C;Genetics:
 A;Gene: SPDB:SPAC637.07; MOB1
 A;Map position: 1
 C;Function:
 A;Description: a component of the Ras1 pathway necessary for proper spindle formation in
 A;Note: Moel and Scd1 interact directly in vitro; it is hypothesized that Scd1 is essent

Query Match 100.0%; Score 31; DB 2; Length 567;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
 |||||
 Db 125 VQGGGR 130

RESULT 6

A45226
 integrin alpha-1 chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
 C;Accession: A45226
 R;Briesewitz, R.; Epstein, M.R.; Marcantonio, E.E.
 J. Biol. Chem. 268, 2989-2996, 1993
 A;Title: Expression of native and truncated forms of the human integrin alpha 1 subunit.
 A;Reference number: A45226; MUID:93155124; PMID:8428973
 A;Accession: A45226
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1151 <BRI>
 A;Experimental source: hepatoblastoma cell line HepG2
 A;Note: sequence extracted from NCBI backbone (NCBIP:124326)
 F142-317/Domain: von Willebrand factor type A repeat homology <VWAL>

Query Match 100.0%; Score 31; DB 2; Length 1151;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
 |||||
 Db 213 VQGGGR 218

RESULT 7

T31318
 hypothetical protein - Cenarchaeum symbiosum
 C;Species: Cenarchaeum symbiosum
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C;Accession: T31318
 R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
 J. Bacteriol. 180, 5003-5009, 1998
 A;Title: Genomic analysis reveals chromosomal variation in natural populations of the ur
 A;Reference number: 220994; MUID:98422450; PMID:9748430
 A;Accession: T31318
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA

A;Residues: 1-269 <SCH>
A;Cross-references: EMBL:AF083072; NID:g3599993; PID:g35999404; PIDN:AAC62709.1

Query Match 96.8%; Score 30; DB 2; Length 269;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGG 6
:|||||
Db 55 IORGG 60

RESULT 8
T09701
phytochrome - Scotch pine
C;Species: Pinus sylvestris (Scotch pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T09701
R;Wiegmann-Eirund, C.M.; Kolukiasoglu, H.U.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z16826
A;Accession: T09701
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1131 <WIE>
A;Cross-references: EMBL:X96738; NID:g1237083
A;Experimental source: isolate pSA 5.1
C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;75-587/Domain: phytochrome homology <PHY>
F;332/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 96.8%; Score 30; DB 2; Length 1131;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGG 6
:|||||
Db 82 IORGG 87

RESULT 9
B69156
hypothetical protein MTH430 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: B69156
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
; Ki, S.; Church, G.W.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69156
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-134 <MTH>
A;Cross-references: GB:AE000827; GB:AE000666; NID:g2621489; PIDN:AA884936.1; PID:g262149
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH430
A;Start codon: TTG

Query Match 90.3%; Score 28; DB 2; Length 134;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGG 6
:|||||
Db 108 IORGG 113

RESULT 10

S39652
secretion protein XcpP PA3104 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2000
C;Accession: S39652; H83258
R;Akrim, M.; Bally, M.; Ball, G.; Tommassen, J.; Teerink, H.; Filloux, A.; Lazdunski, A.
Mol. Microbiol. 10, 431-443, 1993
A;Title: Xcp-mediated protein secretion in Pseudomonas aeruginosa: identification of two
A;Reference number: S39652; MUID:95020542; PMID:7934833
A;Accession: S39652
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-235 <AKR>
A;Cross-references: EMBL:X68594; NID:g431183; PIDN:CAA48581.1; PID:g431184
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83258
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-235 <STO>
A;Cross-references: GB:AE004734; GB:AE004091; NID:g9949204; PIDN:AAG06492.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: xcpP; PA3104

Query Match 90.3%; Score 28; DB 2; Length 235;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGG 6
:|||||
Db 154 IORGG 159

RESULT 11
B83462
probable short-chain dehydrogenase PA1470 [imported] - Pseudomonas aeruginosa (strain PA
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Aug-2001
C;Accession: B83462
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83462
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-245 <STO>
A;Cross-references: GB:AE004576; GB:AE004091; NID:g9947415; PIDN:AAG04859.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1470
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 90.3%; Score 28; DB 2; Length 245;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGG 6
:|||||
Db 129 VERGG 134

RESULT 12
D30191
conserved hypothetical protein yviA - Bacillus subtilis
C;Species: Bacillus subtilis

C>Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: I40386; J0191; A70042; S28596
R:Londono-Vallejo, J.A.; Dubnau, D.
Mol. Microbiol. 9, 119-131, 1993
A:Title: comF, a Bacillus subtilis late competence locus, encodes a protein similar to A
A:Reference number: I40386; MUID:94018599; PMID:8412657
A:Molecule type: DNA
A:Accession: I40386
A:Residues: 1-281 <RES>
A:Cross-references: EMBL:Z18629; NID:G39847; PIDN:CAA79225.1; PID:G39848
R:Hanner, D.J.; Yang, M.; Ferrari, E.
J. Bacteriol. 170, S102-S109, 1988
A:Title: Localization of Bacillus subtilis sacU(Hy) mutations to two linked genes with s
A:Reference number: A30191; MUID:8903891; PMID:3141378
A:Accession: D30191
A:Molecule type: DNA
A:Residues: 1-107 <HN>
R:Kunst, F.; Ogasawara, N.; Moser, J.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallie
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y, W.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Segiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.P.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69590; MUID:98044033; PMID:9384377
A:Accession: A70042
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-281 <UN>
A:Cross-references: GB:Z99122; GB:AL009126; NID:G2636029; PIDN:CAB15565.1; PID:G2636074
A:Experimental source: strain 168
C:Genetics:
A:Gene: yviA
C:Superfamily: Mycoplasma hypothetical protein MG326

Query Match 90.3%; Score 28; DB 1; Length 281;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VORGG 6
Db 167 LQGG 172

RESULT 13
AB1389
B. subtilis yviA (DegV) protein homolog lmo2514 [imported] - Listeria monocytogenes (str
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 01-Mar-2002
C:Accession: AB1389
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1389
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD00592.1; PID:G16412002; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:

A:Gene: lmo2514
C:Superfamily: Mycoplasma hypothetical protein MG326

Query Match 90.3%; Score 28; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VORGG 6
Db 169 LQGG 174

RESULT 14
AD1764
B. subtilis yviA (DegV) protein homolog lin2658 [imported] - Listeria innocua (strain CI
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 01-Mar-2002
C:Accession: AD1764
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97884.1; PID:G16415194; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2658
C:Superfamily: Mycoplasma hypothetical protein MG326

Query Match 90.3%; Score 28; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VORGG 6
Db 169 LQGG 174

RESULT 15
A48561
inner capsid protein VP6 - bluetongue virus (serotype 11, strain USA)
C:Species: bluetongue virus
C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 17-Feb-1994
C:Accession: A48561
R:Hwang, G.Y.; Chieu, J.F.; Yang, Y.Y.; Li, J.K.
Virus Res. 24, 315-323, 1992
A:Title: Comparative sequence analyses of the cognate structural protein VP6 genes of fi
A:Reference number: A48561; MUID:93033709; PMID:1329371
A:Accession: A48561
A:Molecule type: Genomic RNA
A:Residues: 1-325 <HWA>
A:Note: sequence extracted from NCBI backbone (NCBIN:115442, NCBIIP:115444)
C:Genetics:
A:Map position: segment 9
C:Superfamily: bluetongue virus VP6 protein
C:Keywords: capsid protein

Query Match 90.3%; Score 28; DB 1; Length 325;
Best Local Similarity 83.3%; Pred. No. 2.3e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VORGG 6
Db 199 VERGG 204

Search completed: April 15, 2004, 10:28:55
JOB time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 10:27:11 ; Search time 11 Seconds
(without alignments)
28.402 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31

Sequence: 1 VQRGGR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------|--------------------|
| 1 | 31 | 100.0 | 567 | 1 IF37_SCHPO | O94236 schizosacch |
| 2 | 31 | 100.0 | 1151 | 1 ITA1_HUMAN | P56199 homo sapien |
| 3 | 30 | 96.8 | 320 | 1 K6PF_VIBPA | Q87kx0 vibrio para |
| 4 | 30 | 96.8 | 320 | 1 K6PF_VIBVU | Q8dcyl vibrio vuln |
| 5 | 30 | 96.8 | 1131 | 1 PHV_PINSY | Q41046 pinus sylve |
| 6 | 28 | 90.3 | 74 | 1 Y350_METKA | Q8tyf0 methanopyru |
| 7 | 28 | 90.3 | 235 | 1 GSPN_PEEAE | Q51575 pseudomonas |
| 8 | 28 | 90.3 | 281 | 1 DEGV_BACSU | P32436 bacillus su |
| 9 | 28 | 90.3 | 283 | 1 YP14_LISMO | Q8y4d5 listeria mo |
| 10 | 28 | 90.3 | 283 | 1 YQ58_LISIN | Q937x9 listeria in |
| 11 | 28 | 90.3 | 301 | 1 PPNK_TROWT | Q83gx6 tropheryma |
| 12 | 28 | 90.3 | 305 | 1 PPNK_TROW8 | Q83ic3 tropheryma |
| 13 | 28 | 90.3 | 325 | 1 VP6_BTIV1 | P32933 bluetongue |
| 14 | 28 | 90.3 | 325 | 1 VP6_BTIV13 | P32934 bluetongue |
| 15 | 28 | 90.3 | 325 | 1 VP6_BTIV17 | P32935 bluetongue |
| 16 | 28 | 90.3 | 329 | 1 VP61_BTIV10 | P23066 bluetongue |
| 17 | 28 | 90.3 | 376 | 1 KITH_HSV23 | P04407 herpes simp |
| 18 | 28 | 90.3 | 550 | 1 PNV_DESGI | Q93177 desulfovibr |
| 19 | 28 | 90.3 | 882 | 1 ENV_SIVM1 | P05885 simian immu |
| 20 | 28 | 90.3 | 907 | 1 IF2_VIBVU | Q8dbw0 vibrio vuln |
| 21 | 28 | 90.3 | 907 | 1 IF2_VIBVY | Q7m109 vibrio vuln |
| 22 | 28 | 90.3 | 1729 | 1 BG11_SCHPO | Q10287 schizosacch |
| 23 | 28 | 90.3 | 1826 | 1 BG33_SCHPO | Q93377 schizosacch |
| 24 | 28 | 90.3 | 1894 | 1 BG52_SCHPO | Q13967 schizosacch |
| 25 | 27 | 87.1 | 88 | 1 RL15_BRANA | P45289 brassica na |
| 26 | 27 | 87.1 | 147 | 1 LD29_PRAE | Q8xnd8 pyroaculum |
| 27 | 27 | 87.1 | 153 | 1 RL15_PIG | P79324 sus scrofa |
| 28 | 27 | 87.1 | 164 | 1 FR1H_RABIT | P25915 cryctolagus |
| 29 | 27 | 87.1 | 165 | 1 RL15_CHICK | P51417 gallus gall |
| 30 | 27 | 87.1 | 173 | 1 FR13_RANCA | P07797 rana catesb |
| 31 | 27 | 87.1 | 174 | 1 FR1L_BOVIN | O46415 bos taurus |
| 32 | 27 | 87.1 | 174 | 1 FR1L_HORSE | P02791 equus cabal |
| 33 | 27 | 87.1 | 174 | 1 FR1L_HUMAN | P02792 homo sapien |

ALIGNMENTS

RESULT 1

IF37_SCHPO STANDARD; PRT; 567 AA.
AC O94236;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Eukaryotic translation initiation factor 3 subunit 7 homolog
DE (Microtubule destabilizing protein moel).
GN MOBI OR SPAC637.07.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=99110922; PubMed=9892665;
RA Chen C.-R., Li Y.-C., Chen J., Hou M.-C., Papadaki P., Chang E.C.;
RT "Moel, a conserved protein in Schizosaccharomyces pombe, interacts
RT with a Ras effector, Scd1, to affect proper spindle formation.";
RL proc. Natl. Acad. Sci. U.S.A. 96:517-522(1999).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
EX Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Gobie A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds R., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Mostl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehtsch H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerrutti L., Lowe J., McCombie W.R., Paulsen I., Potashkin J.,
RA Spakovskii G.V., Uesery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
[3]
RN FUNCTION.
RX MEDLINE=21648721; PubMed=11705997;
RA Bandyopadhyay A., Lakshmanan V., Matsumoto T., Chang E.C., Maitra U.;

34 27 87.1 174 1 FR1L_RABIT P09451 cryctolagus
35 27 87.1 177 1 FR1H_SALSA P49946 salmo salar
36 27 87.1 179 1 FR1H_CHICK P08267 gallus gall
37 27 87.1 180 1 FR1H_BOVIN O46414 bos taurus
38 27 87.1 181 1 FR1H_MOUSE P09528 mus musculus
39 27 87.1 181 1 FR1H_RAT F19332 rattus norv
40 27 87.1 182 1 FR1H_HUMAN P02794 homo sapien
41 27 87.1 182 1 SRPB_SYN7 Q9xt73 trichosurus
42 27 87.1 182 1 SRPB_SYN7 Q55026 synchococc
43 27 87.1 185 1 FR1H_CRIGR P29389 cricetulus
44 27 87.1 194 1 R15E_PVRAB Q9v032 pyrococcus
45 27 87.1 194 1 R15E_PVRHO O58706 pyrococcus

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RT "Moel and spint6, the fission yeast homologues of mammalian
RT translation initiation factor 3 subunits p66 (eIF3d) and p48 (eIF3e),
RT respectively, are required for stable association of eIF3 subunits.";
RL J. Biol. Chem. 277:2360-2367(2002)
CC -!- FUNCTION: Binds to the 40S ribosome. Induces instability in
CC microtubules. Affect spiggle formation.
CC -!- SUBUNIT: Associates with prt1 subunit of eIF3. Interacts with
CC scd1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE EIF37 FAMILY.
CC -----
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CC -----
DR EMBL; AF038568; AAC08893.1; -
DR EMBL; AL034583; CAA22586.1; -
DR PIR; T43555; T43555.
DR GeneDB SPombe; SPAC637.07; -.
DR InterPro; IPR007783; EIF-3 zeta.
DR Pfam; PF05091; eIF-3 zeta.1.
KW Nuclear protein; Initiation factor; Protein biosynthesis.
FT CONFLICT 367 367 Q -> E (IN REF. 2).
SQ SEQUENCE 567 AA; 62636 MW; 5C382CAV54A747D1 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 567;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
DB 125 VQGGGR 130
|||||

RESULT 2
ITAL HUMAN STANDARD; PRT; 1151 AA.
AC P56199;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Integrin alpha-1 (Laminin and collagen receptor) (VLA-1) (CD49a).
GN ITGAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9315124; PubMed=8428973;
RA Briesewitz R.; Epstein M.R.; Marcantonio E.E.;
RT "Expression of native and truncated forms of the human integrin alpha
RT 1 subunit.";
RL J. Biol. Chem. 268:2989-2996(1993).
RC -!- FUNCTION: INTEGRIN ALPHA-1/BETA-1 IS A RECEPTOR FOR LAMININ AND
CC COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-P-P-G-
CC E-R IN COLLAGEN.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1
CC ASSOCIATES WITH BETA-1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
CC WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: NAME=PROV; NOTE=CD guide CD49a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd49a.htm".
DR PIR; A45226; A45226.
DR PDB; 1QC5; 17-MAY-00.

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DR Genew; HGNC:6134; ITGAL.
DR MIM; 192968; -.
DR GO; GO:0008305; C: integrin complex; TAS.
DR GO; GO:0004895; F: cell adhesion receptor activity; NAS.
DR GO; GO:0005518; F: collagen binding; TAS.
DR GO; GO:0007160; P: cell-matrix adhesion; NAS.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWFA.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_A; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWFA_1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS00234; VWFA; 1.
DR Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW Repeat; Calcium; Magnesium; 3D-structure.
FT DOMAIN 1 113
FT TRANSMEM 114 1136
FT DOMAIN 117 1151
FT REPEAT 16 75
FT REPEAT ?
FT DOMAIN 147 360
FT REPEAT 349 404
FT REPEAT 405 457
FT REPEAT 459 520
FT REPEAT 540 599
FT REPEAT 602 654
FT CA_BIND 470 478
FT CA_BIND 552 560
FT CA_BIND 614 622
FT SITE 1139 1142
FT DISULFID 54 64
FT DISULFID 650 669
FT DISULFID 675 728
FT DISULFID 780 786
FT DISULFID 850 858
FT DISULFID 1002 1034
FT DISULFID 1037 1044
FT CARBOHYD 46 46
FT CARBOHYD 72 72
FT CARBOHYD 77 77
FT CARBOHYD 84 84
FT CARBOHYD 189 189
FT CARBOHYD 289 289
FT CARBOHYD 313 313
FT CARBOHYD 374 374
FT CARBOHYD 390 390
FT CARBOHYD 432 432
FT CARBOHYD 504 504
FT CARBOHYD 671 671
FT CARBOHYD 720 720
FT CARBOHYD 752 752
FT CARBOHYD 812 812
FT CARBOHYD 855 855
FT CARBOHYD 880 880
FT CARBOHYD 911 911
FT CARBOHYD 938 938
FT CARBOHYD 946 946
FT CARBOHYD 980 980
FT CARBOHYD 1045 1045
FT CARBOHYD 1055 1055
FT CARBOHYD 1074 1074
FT CARBOHYD 1085 1085
SQ SEQUENCE 1151 AA; 127837 MW; 6B3F3C1AABF52808 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 1151;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
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Db          213 VQRGR 218

RESULT 3
K6PF_VIBPA STANDARD; PRT; 320 AA.
AC Q87KK0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE (Phosphohexokinase).
GN PFKA OR VF2855.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]_SIMILARITY: Belongs to the phosphofructokinase family.
RP SEQUENCE FROM N.A.
RC STRAIN=RMND 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
CC -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -!- PATHWAY: Key control step of glycolysis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the phosphofructokinase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF005083; BAC61118.1; -.
CC HAMAP; MF 00339; -; 1.
CC InterPro; IPR000023; Pfpruckinase.
CC Pfam; PF00365; PFK; 1.
CC PRINTS; PR00476; PHFRCTKINASE.
CC PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
CC KINASE; Transferase; Glycolysis; Complete proteome.
CC SQ SEQUENCE 320 AA; 34592 MW; A39DEF12B37AF211 CRC64;

Query Match          96.8%; Score 30; DB 1; Length 320;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 VQRGR 6
DB          251 IQRGR 256

RESULT 4
K6PF_VIBVU STANDARD; PRT; 320 AA.
AC Q8DCY1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE (Phosphohexokinase).
GN PFKA OR V11257.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;

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RN SEQUENCE FROM N.A.
RP STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -!- PATHWAY: Key control step of glycolysis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the phosphofructokinase family.
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CC -----
CC EMBL; AE016801; AAC09713.1; -.
CC HAMAP; MF 00339; -; 1.
CC InterPro; IPR000023; Pfpruckinase.
CC Pfam; PF00365; PFK; 1.
CC PRINTS; PR00476; PHFRCTKINASE.
CC PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
CC KINASE; Transferase; Glycolysis; Complete proteome.
CC SQ SEQUENCE 320 AA; 34469 MW; 29515DB431453901 CRC64;

Query Match          96.8%; Score 30; DB 1; Length 320;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 VQRGR 6
DB          251 IQRGR 256

RESULT 5
PHY_PINSY STANDARD; PRT; 1131 AA.
ID PHY_PINSY
AC Q41046;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phytochrome.
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3349;
RN [1]_SIMILARITY: Belongs to the phytochrome family.
RP SEQUENCE FROM N.A.
RC STRAIN=PSA 5.1;
RX MEDLINE=99408267; PubMed=10480390;
RA Clapham D.H., Kolukisaoglu H.U., Larsson C.T., Qamaruddin M.,
RA Eberg I., Wiegmann-Birund C., Schneider-Poetsch H.A., von Arnold S.;
RT "Phytochrome types in Picea and Pinus. Expression patterns of
RT P1A-related types."
RL Plant Mol. Biol. 40:669-678(1999).
CC -!- FUNCTION: Regulatory photoreceptor which exists in two forms that
CC are reversibly interconvertible by light; the Pr form that absorbs
CC maximally in the red region of the spectrum and the Pfr form that
CC absorbs maximally in the far-red region. Photoconversion of Pr in
CC Pfr induces an array of morphogenic responses, whereas
CC reconversion of Pfr to Pr cancels the induction of those
CC responses. Pfr controls the expression of a number of nuclear
CC genes including those encoding the small subunit of ribulose-
CC biphosphate carboxylase, chlorophyll A/B binding protein,
CC protochlorophyllide reductase, rRNA, etc. It also controls the
CC expression of its own gene(s) in a negative feedback fashion.
CC -!- SUBUNIT: Homodimer (By similarity).

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CC -!- PTM: Contains one covalently linked tetrapyrrole chromophore.
 CC -!- SIMILARITY: Belongs to the phytochrome family.
 CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -----
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 CC -----
 CC EMBL; X96738; CAA63510.1; -;
 DR PIR; T09701; T09701.
 DR InterPro; IPR003594; APPbind_ATPase.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR003661; His_KinA_N.
 DR InterPro; IPR005467; His_Kinase.
 DR InterPro; IPR001610; PAC_domain.
 DR InterPro; IPR000014; PAS_domain.
 DR InterPro; IPR001294; Phytochrome.
 DR Pfam; PF01590; GAF; 1.
 DR Pfam; PF02519; HATPase_c; 1.
 DR Pfam; PF00512; Hiska; 1.
 DR Pfam; PF00989; PAS; 2.
 DR Pfam; PF00360; Phytochrome; 1.
 DR PRINTS; PR01033; PHYTOCHROME.
 DR SMART; SM00065; GAF; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; Hiska; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR TIGRFAMs; TIGR00229; sensory_box; 2.
 DR PROSITE; PS50109; HIS_KIN; 1.
 DR PROSITE; PS0112; PAS; 2.
 DR PROSITE; PS00245; PHYTOCHROME_1; 1.
 DR PROSITE; PS50046; PHYTOCHROME_2; 1.
 KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
 KW Repeat.
 FT DOMAIN 621 692 PAS 1.
 FT DOMAIN 755 826 PAS 2.
 FT DOMAIN 903 1123 HISTIDINE KINASE.
 FT BINDING 332 332 CHROMOPHORE (BY SIMILARITY).
 SQ SEQUENCE 1131 AA; 126254 MW; D63A2008FA9862FB CRC64;
 Query Match 96.8%; Score 30; DB 1; Length 1131;
 Best Local Similarity 83.3%; Pred. No. 95;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQRGGR 6
 Db 82 IQRGR 87
 RESULT 6
 Y350 METKA
 ID Y350 METKA STANDARD; PRT; 74 AA.
 AC Q8TVF0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Hypothetical UPF0248 protein MK0350.
 GN MK0350.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus
 OC Methanopyrus
 OX NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014;

RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozvavkin S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 RT and monophyly of archaeal methanogens".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 CC -!- SIMILARITY: Belongs to the UPF0248 family.
 CC -----
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 CC -----
 CC EMBL; AE010332; AM01565.1; -;
 DR HAMAP; MF_01245; -; 1.
 DR InterPro; IPR007547; DUF504.
 DR Pfam; PF04457; DUF504; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 74 AA; 8739 MW; D033CA40786A1B96 CRC64;
 Query Match 90.3%; Score 28; DB 1; Length 74;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQRGGR 6
 Db 56 VERGGR 61
 RESULT 7
 GSPN_PSEAE
 ID GSPN_PSEAE STANDARD; PRT; 235 AA.
 AC Q51575; Q9HZR3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE General secretion pathway protein N (XcpP protein).
 GN XCPP OR PA3104.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=95020542; PubMed=7934833;
 RA Akrim M., Bally M., Ball G., Tomassen J., Teerink H., Filloux A.,
 RA Lazdunski A.;
 RT "Xcp-mediated protein secretion in Pseudomonas aeruginosa:
 RT identification of two additional genes and evidence for regulation of
 RT xcp gene expression.";
 RL Mol. Microbiol. 10:431-443 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 RN [3]
 RP SUBCELLULAR LOCATION, AND TOPOLOGY.
 RX MEDLINE=96312375; PubMed=8763961;
 RA Bleves S., Lazdunski A., Filloux A.;

RT "Membrane topology of three Xcp proteins involved in exoprotein
 RL transport by *Pseudomonas aeruginosa*.";
 CC J. Bacteriol. 178:4297-4300(1996).
 CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
 CC EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF A VARIETY
 CC OF ENZYMES ACROSS THE OUTER MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
 CC
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 CC
 CC EMBL: X68594; CAA48581.1; -;
 CC EMBL: AB004734; AAG06492.1; -;
 CC PIR: S39652; S39652.
 CC Inner membrane; Transmembrane; Transport; Signal-anchor;
 CC Complete proteome.
 CC
 CC DOMAIN 1 34 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 35 55 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC FT TRANSMEM 35 55 PERIPLASMIC (POTENTIAL).
 CC FT DOMAIN 56 235 PERIPLASMIC (POTENTIAL).
 CC FT SEQUENCE 235 AA; 25496 MW; DE926984D89A0D7 CRC64;
 CC
 CC Query Match 90.3%; Score 28; DB 1; Length 235;
 CC Best Local Similarity 83.3%; Pred. No. 53;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 VORGG 6
 CC :|||||
 CC Db 154 LORGG 159
 CC
 CC RESULT 8
 CC DEGV BACSU
 CC ID DEGV BACSU STANDARD; PRT; 281 AA.
 CC AC P22436;
 CC DT 01-OCT-1993 (Rel. 27, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Degv protein.
 CC GN DEGV OR BSU35480.
 CC OS Bacillus subtilis.
 CC OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CC OX NCBI_TaxID=1423;
 CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RP STRAIN=168;
 CC RX MEDLINE=94018599; PubMed=8412657;
 CC RA Londono-Vallejo J.A., Dubnau D.;
 CC "comp", a Bacillus subtilis late competence locus, encodes a protein
 CC similar to ATP-dependent RNA/DNA helicases.";
 CC RL Mol. Microbiol. 9:119-131(1993).
 CC [2]
 CC RN SEQUENCE FROM N.A.
 CC RP STRAIN=168;
 CC RX MEDLINE=98044033; PubMed=9384377;
 CC RA Kunet F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 CC Azevedo V., Bertoletti M., Bessieres P., Bolotin A., Borchert S.,
 CC Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 CC Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 CC Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 CC Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 CC

RA Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Haich J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kaashara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidas A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,
 RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudaga B., Park S.H.,
 RA Parro V., Pohl T.M., Portetle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purrelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 CC "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 CC *subtilis*".
 CC RL Nature 390:249-256(1997).
 CC [4]
 CC RN SEQUENCE OF 1-107 FROM N.A.
 CC RX MEDLINE=89033891; PubMed=3141378;
 CC RA Henner D.J., Yang M., Ferrari E.;
 CC "Localization of *Bacillus subtilis* sacU(Hv) mutations to two linked
 CC genes with similarities to the conserved procaryotic family of two-
 CC component signalling systems".
 CC J. Bacteriol. 170:5102-5109(1988).
 CC -1- SIMILARITY: BELONGS TO THE UPF0230 (DEGV) FAMILY.
 CC
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 CC
 CC EMBL: Z18629; CAA79225.1; -;
 CC EMBL: U58903; AAC44939.1; -;
 CC EMBL: Z99122; CAB15565.1; -;
 CC EMBL: M23558; -; NOT_ANNOTATED_CDS.
 CC PIR: I40386; D30191.
 CC DR SubtilList; BG10394; degv.
 CC DR InterPro; IPR003797; Degv.
 CC Pfam; PF02645; DUF194; 1.
 CC TIGRFAMs; TIGR00762; Degv; 1.
 CC Complete proteome.
 CC
 CC Query Match 90.3%; Score 28; DB 1; Length 281;
 CC Best Local Similarity 83.3%; Pred. No. 64;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 VORGG 6
 CC :|||||
 CC Db 167 LORGG 172
 CC
 CC RESULT 9
 CC IPI4 LISMO
 CC ID IPI4 LISMO STANDARD; PRT; 283 AA.
 CC AC Q8Y4D5;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Hypothetical UPF0230 protein lmo2514.
 CC LMO2514.

```

OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Enriani K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Jopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- SIMILARITY: BELONGS TO THE UPF0230 (DEGV) FAMILY.
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CC -----
CC EMBL; AL591983; CAD00592.1; --
CC PIR; ABL1389; ABL1389.
CC ListList; LMO02514; --
CC InterPro; IPR003797; DegV.
CC Pfam; PF02645; DUF194; 1.
CC TIGRFAMs; TIGR00762; DegV; 1.
CC KW Hypothetical protein; Complete proteome.
CC SEQUENCE 283 AA; 31257 MW; 2676C2CF7D2666C CRC64;
CC -----
CC Query Match 90.3%; Score 28; DB 1; Length 283;
CC Best Local Similarity 83.3%; Pred. No. 64;
CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 1 VORGG 6
CC Db 169 LQGG 174
CC -----
RESULT 11
PPNK_TROWT STANDARD; PRT; 301 AA.
AC Q83GX6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)
DE [Poly(P)/ATP NAD Kinase].
GN PPNK OR TW103.
OS Tropheryma whipplei (strain Twist) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22784088; PubMed=12902375;
RA Racult D., Ogata H., Audic S., Robert C., Suhr K., Drancourt M.,
RA Claverie J.-M.;
RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
RT reduced genome.";
RL Genome Res. 13:1800-1809(2003).
CC -!- FUNCTION: Catalyzes the phosphorylation of NAD to NADP. Utilizes
CC ATP and other nucleoside triphosphates as well as inorganic
CC polyphosphate as a source of phosphorus (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + NAD(+) = ADP + NADP(+).
CC -!- COFACTOR: Divalent metal ions (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the NAD kinase family.
CC -----
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CC -----
CC EMBL; AE016850; AA044200.1; --
CC HAMAP; MF 00361; -- 1.
CC InterPro; IPR002504; ATP_NADK.

```

DR Pfam; PF01513; NAD_kinase; 1.
 KW Transferase; Kinase; NAD; Complete proteome.
 SQ SEQUENCE 301 AA; 32917 MW; E44153CD31FEB99 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 301;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
 Db 144 VQGGGK 149
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RESULT 12
 ID PF01513 TROW8 STANDARD; PRT; 305 AA.
 AC Q831C3;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)
 DE (Poly(P)/ATP NAD kinase).
 GN PF01513
 OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcales; Cellulomonadaceae; Tropheryma.
 OX NCBI_TaxID=218496;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22495039; PubMed=12606174;
 RA Bentley S.D., Mairwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
 RA Dover L.G., Norbertzak H.T., Besra G.S., Quail M.A., Harris D.E.,
 RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
 RA Barrall B.G., Parkhill J., Reiman D.A.;
 RT "Sequencing and analysis of the genome of the Whipple's disease
 bacterium Tropheryma whipplei";
 RL Lancet 361:637-644(2003).
 CC -!- FUNCTION: Catalyzes the phosphorylation of NAD to NADP. Utilizes
 CC ATP and other nucleoside triphosphates as well as inorganic
 CC polyphosphate as a source of phosphorus (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + NAD(+) = ADP + NADP(+).
 CC -!- COPACATOR: Divalent metal ions (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the NAD kinase family.

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 CC -----

EMBL; BX251410; CAD66795.1; -;
 DR HAMAP; MF_00361; -; 1.
 DR InterPro; IPR002504; ATP_NADK.
 DR Pfam; PF01513; NAD_kinase; 1
 KW Transferase; Kinase; NAD; NADP; Complete proteome.
 SQ SEQUENCE 305 AA; 33273 MW; C53563B959052ESD CRC64;

Query Match 90.3%; Score 28; DB 1; Length 305;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
 Db 148 VQGGGK 153
 |||||

RESULT 13
 ID VP6_BT11
 AC P32933;
 STANDARD; PRT; 325 AA.

DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DS VP6 protein (Minor inner core protein VP6).
 S9.
 GN Bluetongue virus (serotype 11 / isolate USA).
 OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
 OX NCBI_TaxID=33716;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93033709; PubMed=1329371;
 RA Hwang G.-Y., Chlou J.-F., Yang Y.-Y., Li J.K.-K.;
 RT "Comparative sequence analyses of the cognate structural protein VP6
 RT genes of five US bluetongue viruses.";
 RL Virus Res. 24:315-323(1992).
 CC -!- FUNCTION: SURROUNDS AND INTERACTS WITH THE GENOMIC DS-RNA.
 CC POSSESSES SS- AND DS-RNA-BINDING CAPACITY. ITS HYDROPHILIC
 CC NATURE AND CAPABILITY TO BIND SS- AND DS-RNA SUGGEST ITS
 CC INTERACTIONS WITH BTV GENOMIC RNA.
 CC -!- SUBCELLULAR LOCATION: Inner capsid.
 CC -!- SIMILARITY: Belongs to the reoviruses VP6 family.

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 CC -----

EMBL; L08670; AAA42819.1; -;
 DR PIR; A48561; A48561.
 DR InterPro; IPR001399; Orbi_VP6.
 DR Pfam; PF01516; Orbi_VP6; 1.
 DR PRINTS; PR00902; VP6CAPSID.
 KW Core protein.84 125 GLY-RICH.
 FT DOMAIN 84 125
 SQ SEQUENCE 325 AA; 35371 MW; 4F189625674B6929 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 325;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGGR 6
 Db 199 VQGGGR 204
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RESULT 14
 ID VP6_BT13
 AC P32934;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VP6 protein (Minor inner core protein VP6).
 S9.
 GN Bluetongue virus (serotype 13 / isolate USA).
 OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
 OX NCBI_TaxID=33717;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93033709; PubMed=1329371;
 RA Hwang G.-Y., Chlou J.-F., Yang Y.-Y., Li J.K.-K.;
 RT "Comparative sequence analyses of the cognate structural protein VP6
 RT genes of five US bluetongue viruses.";
 RL Virus Res. 24:315-323(1992).
 CC -!- FUNCTION: SURROUNDS AND INTERACTS WITH THE GENOMIC DS-RNA.
 CC POSSESSES SS- AND DS-RNA-BINDING CAPACITY. ITS HYDROPHILIC
 CC NATURE AND CAPABILITY TO BIND SS- AND DS-RNA SUGGEST ITS
 CC INTERACTIONS WITH BTV GENOMIC RNA.
 CC -!- SUBCELLULAR LOCATION: Inner capsid.
 CC -!- SIMILARITY: Belongs to the reoviruses VP6 family.

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CC -----
DR EMBL; L08671; AAA42820.1; ..
DR InterPro; IPR001399; Orbi.VP6.
DR Pfam; PF01516; Orbi.VP6; 1.
DR PRINTS; PR00902; VP6CAPSID.
KW Core protein.
FT DOMAIN 84 125 GLY-RICH.
SQ SEQUENCE 325 AA; 35245 MW; F084DB712702A334 CRC64;
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Query Match 90.3%; Score 28; DB 1; Length 325;
Best Local Similarity 83.3%; Pred.No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRGGR 6
Db 199 VERGGR 204
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RESULT 15
VP6_BT17
ID_VP6_BT17 STANDARD; PRT; 325 AA.
AC P32935;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VP6 protein (Minor inner core protein VP6).
GN S9.
OS Bluetongue virus (serotype 17 / isolate USA).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=33718;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93033709; PubMed=1329371;
RA Hwang G.-Y., Chiou J.-F., Yang Y.-Y., Li J.K.-K.;
RT "Comparative sequence analyses of the cognate structural protein VP6
RT Genes of five US bluetongue viruses.";
RL Virus Res. 24:315-323(1992).
CC -!- FUNCTION: SURROUNDS AND INTERACTS WITH THE GENOMIC DS-RNA.
CC POSSESSES SS- AND DS-RNA-BINDING CAPACITY. ITS HYDROPHILIC
CC NATURE AND CAPABILITY TO BIND SS- AND DS-RNA SUGGEST ITS
CC INTERACTIONS WITH BTV GENOMIC RNA.
CC -!- SUBCELLULAR LOCATION: Inner capsid.
CC -!- SIMILARITY: Belongs to the reoviruses VP6 family.
CC -----
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CC -----
DR EMBL; L08672; AAA42821.1; ..
DR InterPro; IPR001399; Orbi.VP6.
DR Pfam; PF01516; Orbi.VP6; 1.
DR PRINTS; PR00902; VP6CAPSID.
KW Core protein.
FT DOMAIN 84 125 GLY-RICH.
SQ SEQUENCE 325 AA; 35317 MW; 650C5986A2DA11C1 CRC64;
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Query Match 90.3%; Score 28; DB 1; Length 325;
Best Local Similarity 83.3%; Pred.No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRGGR 6
```

```
Db 199 VERGGR 204
```

```
Search completed: April 15, 2004, 10:29:19
Job time : 12 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 10:27:11 ; Search time 39 Seconds
(without alignments)
48.541 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31

Sequence: 1 VQRGR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mic.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 31 | 100.0 | 96 | 15 O91897 | O91897 human immun |
| 2 | 31 | 100.0 | 114 | 2 Q7482 | Q7482 escherichia |
| 3 | 31 | 100.0 | 138 | 10 Q8H2B8 | Q8H2B8 anacardium |
| 4 | 31 | 100.0 | 169 | 10 Q8LPD4 | Q8LPD4 linum usita |
| 5 | 31 | 100.0 | 200 | 11 Q8CCZ7 | Q8CCZ7 mus musculus |
| 6 | 31 | 100.0 | 200 | 15 Q8P408 | Q8P408 xanthomonas |
| 7 | 31 | 100.0 | 244 | 16 Q8A4X1 | Q8A4X1 bacteroides |
| 8 | 31 | 100.0 | 278 | 2 Q07397 | Q07397 mycobacteri |
| 9 | 31 | 100.0 | 351 | 16 Q8UAR6 | Q8UAR6 agrobacteri |
| 10 | 31 | 100.0 | 394 | 2 Q4416 | Q4416 agrobacteri |
| 11 | 31 | 100.0 | 424 | 16 Q883U6 | Q883U6 rhizobium 1 |
| 12 | 31 | 100.0 | 730 | 5 Q8SUE4 | Q8SUE4 encephalito |
| 13 | 30 | 96.8 | 130 | 1 Q8UWU6 | Q8UWU6 sulfolobus |
| 14 | 30 | 96.8 | 131 | 16 Q89DF0 | Q89DF0 brachyrhizob |
| 15 | 30 | 96.8 | 170 | 5 Q8T312 | Q8T312 suberites d |
| 16 | 30 | 96.8 | 269 | 1 O74066 | O74066 cenarchaeum |

| | | | | | |
|----|----|------|-----|-----------|---------------------|
| 17 | 30 | 96.8 | 273 | 1 O74043 | O74043 cenarchaeum |
| 18 | 30 | 96.8 | 273 | 16 Q9ADNO | Q9ADNO streptomyce |
| 19 | 30 | 96.8 | 854 | 2 Q846Q2 | Q846Q2 myxococcus |
| 20 | 28 | 90.3 | 72 | 2 Q93N80 | Q93N80 streptomyce |
| 21 | 28 | 90.3 | 81 | 16 Q8RLG8 | Q8RLG8 corynebacte |
| 22 | 28 | 90.3 | 120 | 11 Q8C9MS | Q8C9MS mus musculu |
| 23 | 28 | 90.3 | 125 | 16 Q8PFWS | Q8PFWS xanthomonas |
| 24 | 28 | 90.3 | 134 | 17 Q26530 | Q26530 methanobact |
| 25 | 28 | 90.3 | 141 | 4 Q9BX98 | Q9BX98 homo sapien |
| 26 | 28 | 90.3 | 168 | 10 Q8LPD3 | Q8LPD3 linum usita |
| 27 | 28 | 90.3 | 206 | 10 Q7XQX8 | Q7XQX8 cryza sativ |
| 28 | 28 | 90.3 | 212 | 10 Q94JK9 | Q94JK9 cryza sativ |
| 29 | 28 | 90.3 | 221 | 10 Q8L4Y4 | Q8L4Y4 cryza sativ |
| 30 | 28 | 90.3 | 225 | 10 Q7XZ97 | Q7XZ97 griffithsia |
| 31 | 28 | 90.3 | 245 | 16 Q913P2 | Q913P2 pseudomonas |
| 32 | 28 | 90.3 | 257 | 16 Q88E85 | Q88E85 pseudomonas |
| 33 | 28 | 90.3 | 258 | 16 Q8F073 | Q8F073 leptospira |
| 34 | 28 | 90.3 | 262 | 16 Q87Y92 | Q87Y92 pseudomonas |
| 35 | 28 | 90.3 | 279 | 16 Q8ENG5 | Q8ENG5 oceanobacill |
| 36 | 28 | 90.3 | 280 | 2 Q8VQ59 | Q8VQ59 bacillus li |
| 37 | 28 | 90.3 | 280 | 16 Q81X19 | Q81X19 bacillus an |
| 38 | 28 | 90.3 | 280 | 16 Q815G1 | Q815G1 bacillus ce |
| 39 | 28 | 90.3 | 281 | 16 Q87MG8 | Q87MG8 vibrio para |
| 40 | 28 | 90.3 | 286 | 16 Q7U4Y7 | Q7U4Y7 synecococc |
| 41 | 28 | 90.3 | 299 | 3 Q9HGL5 | Q9HGL5 schizosacch |
| 42 | 28 | 90.3 | 326 | 1 Q9HH16 | Q9HH16 methanosarc |
| 43 | 28 | 90.3 | 329 | 12 Q96661 | Q96661 bluetongue |
| 44 | 28 | 90.3 | 329 | 12 Q96659 | Q96659 bluetongue |
| 45 | 28 | 90.3 | 329 | 12 Q96656 | Q96656 bluetongue |

ALIGNMENTS

RESULT 1

O91897 ID O91897 PRELIMINARY; PRT; 96 AA.
AC O91897;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
GN Vpr protein.
GN VPR.
CS Human immunodeficiency virus 1.
CC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CG30.5;
RA Moriyama H.;
RT "HIV-1 in Congo."
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF056186; AAC61996.1;
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR: 1.
DR PRINTS; PR00444; HIVPRVPRX.
KW AIDS.
SQ SEQUENCE 96 AA; 11265 MW; 43EBFAS7BED84D7 CRC64;

Query Match 100.0%; Score 31; DB 15; Length 96;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRGR 6
|||
DB 85 VQRGR 90

RESULT 2

Q47482 ID Q47482 PRELIMINARY; PRT; 114 AA.
AC Q47482;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ORF114.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=30170953; PubMed=2155230;
 RA "Chen C.-M., Ye Q.-Z., Zhu Z., Wanner B.L., Walsh C.T.;
 RT "Molecular biology of carbon-phosphorus bond cleavage: Cloning and
 RT sequencing of the phn (psd) genes involved in alkyphosphonate uptake
 RT and C-P lyase activity in Escherichia coli B.";
 RL J. Biol. Chem. 265:4461-4471(1990).
 DR EMBL; J05260; AAA24351.1; -.
 DR PIR; C35720; C35720.
 SQ SEQUENCE 114 AA; 12496 MW; P754EC426153011A CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQRGR 6
 Db 40 VQRGR 45
 RESULT 3
 Q8H2B8 PRELIMINARY; PRT; 138 AA.
 AC Q8H2B8
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 2s albumin.
 GN ANA O 3.
 OS Anacardium occidentale (cashew).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Sapindales; Anacardiaceae; Anacardium.
 OX NCBI_TaxID=171929;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Wang F., Roux K.H., Teuber T.S., Sathe S.K.;
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY081853; AAL91665.1; -.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR Pfam; PF00234; tryp_alpha_aml1; 1.
 DR PRINTS; PR00496; NAFIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 138 AA; 16335 MW; 63BB43544BD46999 CRC64;
 Query Match 100.0%; Score 31; DB 10; Length 138;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQRGR 6
 Db 60 VQRGR 65
 RESULT 4
 Q8LPD4 PRELIMINARY; PRT; 169 AA.
 ID Q8LPD4
 AC Q8LPD4
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Conlinin.
 GN CNL1.

OS Linum usitatissimum (Flax) (Linseed).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Linaceae; Linum.
 OX NCBI_TaxID=4006;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. CDC Normandy;
 RA Truksa M., Mackenzie S.L., Qiu X.;
 RT "Molecular cloning of flax 2S storage protein conlinin and seed
 RT specific activity of its promoter.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ414732; CAC94010.1; -.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR Pfam; PF00234; tryp_alpha_aml1; 1.
 DR PRINTS; PR00496; NAFIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 169 AA; 19063 MW; 1E315E2928596E8B CRC64;
 Query Match 100.0%; Score 31; DB 10; Length 169;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQRGR 6
 Db 72 VQRGR 77
 RESULT 5
 Q8CCZ7 PRELIMINARY; PRT; 200 AA.
 ID Q8CCZ7
 AC Q8CCZ7
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN 630403A02RIK OR R75555.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RL "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK031805; BAC27559.1; -.
 DR PIR; P70649; PT0712.
 DR MGD; MGI:2138735; 6330403A02RIK.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 200 AA; 21017 MW; EE5A99ECC0C8C72A CRC64;
 Query Match 100.0%; Score 31; DB 11; Length 200;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQRGR 6
 Db 74 VQRGR 79
 RESULT 6
 Q8P408 PRELIMINARY; PRT; 200 AA.
 ID Q8P408
 AC Q8P408
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Two-component system regulatory protein.
 GN XCC3909.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=2202145; PubMed=1202417;
 RA da Silva A.C.R., Ferro J.A., Reinach P.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., Monteiro A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."
 RL Nature 417:459-463 (2002).
 DR EMBL; AE012511; AAM4313.1; --
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0000155; F:two-component response regulator activity; IEA.
 DR GO; GO:0000160; F:two-component signal transduction system (p. . .); IEA.
 DR InterPro; IPR000792; HTH LuxR.
 DR Pfam; PF00196; GerE; 1.
 DR Pfam; PF00072; response_reg; 1.
 DR PRINTS; PR00038; HTHLUXR.
 DR ProDom; PD000307; HTH_LuxR; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR PROSITE; PS00110; RESPONSE_REGULATORY; 1.
 KW Complete proteome.
 SQ SEQUENCE 200 AA; 21953 MW; ACD29C7AB8E0179A CRC64;
 Query Match 100.0%; Score 31; DB 16; Length 200;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VQRGGR 6
 Db 118 VQRGGR 123
 ID Q8A4X1 PRELIMINARY; PRT; 244 AA.
 AC Q8A4X1.
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN BT2476.
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
 RL Science 299:2074-2076(2003).
 DR EMBL; AE016936; AA077583.1; --
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR ProDom; PD001677; Ribosomal_L24.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 244 AA; 27020 MW; 5946A88A0EA60D5 CRC64;
 Query Match 100.0%; Score 31; DB 16; Length 244;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VQRGGR 6
 Db 32 VQRGGR 37
 ID Q07397 PRELIMINARY; PRT; 278 AA.
 AC Q07397;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MAV278.
 GN MAV278.
 OS Mycobacterium avium.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GIR10;
 RX MEDLINE=98195739; PubMed=9534249;
 RA Labo M., Gusherti L., Rossi E.D., Speciale P., Riccardi G.;
 RT "Determination of a 15437 bp nucleotide sequence around the inhA gene
 RT of Mycobacterium avium and similarity analysis of the products of
 RT putative ORFs."
 RL Microbiology 144:807-814(1998).
 DR EMBL; AF002133; AAC46201.1; --
 SQ SEQUENCE 278 AA; 30646 MW; AE985A67F9D09D97 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VQRGGR 6
 Db 164 VQRGGR 169
 ID Q8UAR6 PRELIMINARY; PRT; 351 AA.
 AC Q8UAR6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Endoglucanase.
 GN CELC OR ATU3307 OR AGR_L_3023GL.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR002037; Glyco hydro 8.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF01270; Glyco_hydro_8; 1.
DR PRINTS; PR00735; GLHYDELAS8.
SQ SEQUENCE 394 AA; 42958 MW; B90607996BE46858 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.5e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 VORGGG 6
| | | | |
Db 262 VQGGGR 267

RESULT 11

ID Q98BU6 PRELIMINARY; PRT; 424 AA.
AC Q98BU6
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amino transferase, Nifs.
GS MLL5421.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Katanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti".
RL DNA Res 7:331-338(2000).
DR ENBL; AP003006; BAB51876.1; -.
DR HSSP; P77444; IUF9.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase; Complete proteome.
SQ SEQUENCE 424 AA; 46938 MW; 9211C5E265231F1B CRC64;

Query Match 100.0%; Score 31; DB 16; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 VORGGG 6
| | | | |
Db 60 VQGGGR 65

RESULT 12

ID Q8SUE4 PRELIMINARY; PRT; 730 AA.
AC Q8SUE4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein ECU10_0900.
GS ECU10_0900.
OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases

```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillor E., Metenier G., Thamarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Aloui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Entamoeba histolytica cuniculi."
RL Nature 414:450-453(2001).
DR EMBL: AL590449; CAD25809.1; -.
DR InterPro: IPR001279; Bactnase-like.
DR Pfam: PF00753; lactamase_B; 1.
KW Hypothetical protein.
SQ SEQUENCE 730 AA; 82037 MW; 6113332D3450F786 CRC64;

Query Match 100.0%; Score 31; DB 5; Length 730;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
Db 312 VORGR 317

RESULT 13
Q9UWU6 PRELIMINARY; PRT; 130 AA.
AC Q9UWU6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORF-C22_010.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1617 / P2;
RA Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
RA Confalonieri P., Curtis B., Duguet M., Etrauso G., Raguy D.,
RA Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
RA Kishwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,
RA St Jean A., Van Der Oost J., Young F., Zivanovic Y., Doellittle W.F.,
RA Ragan M.A., Sensen C.W.;
RT "Gene content and organization of a 281-kbp contig from the genome of
RT the extremely thermophilic archaeon, Sulfolobus solfataricus P2."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y18930; CAB57758.1; -.
KW Hypothetical protein.
SQ SEQUENCE 130 AA; 14047 MW; 94B19DA20F333197 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 130;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
Db 109 IORGR 114

RESULT 14
Q89DF0 PRELIMINARY; PRT; 131 AA.
AC Q89DF0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lactoylglutathione lyase.
GN LGUL OR BLR7489.

OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasanoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Isumoto H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL: AP005962; BAC52754.1; -.
DR GO: GO:0016829; F-lyase activity; IEA.
DR InterPro: IPR004360; Gly_dio_x.
DR Pfam: PF00903; Glyoxalase; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 131 AA; 15057 MW; 3B9272DDA89C4FC9 CRC64;

Query Match 96.8%; Score 30; DB 16; Length 131;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
Db 124 IORGR 129

RESULT 15
Q8T312 PRELIMINARY; PRT; 170 AA.
AC Q8T312;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferritin type 2.
GN FTN2.
OS Suberites domuncula (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Hadromerida; Suberitidae; Suberites.
OX NCBI_TaxID=55567;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21869339; PubMed=11879581;
RA Krasko A., Schroeder H.C., Batel R., Grebenjuk V.A., Steffen R.,
RA Mueller I.M., Mueller W.E.G.;
RT "Iron induces proliferation and morphogenesis in primmorphs from the
RT marine sponge Suberites domuncula."
RL DNA Cell Biol. 21:67-80(2002).
DR EMBL: AJ306614; CAC84555.1; -.
DR GO: GO:0005488; F-binding; IEA.
DR GO: GO:0008199; F-iron ion binding; IEA.
DR GO: GO:0006879; P-iron ion homeostasis; IEA.
DR GO: GO:0008826; P-iron ion transport; IEA.
DR InterPro: IPR001519; Ferritin.
DR InterPro: IPR008331; Ferritin_Dps.
DR Pfam: PF00210; ferritin; 1.
DR ProDom: PD000971; Ferritin; 1.
DR PROSITE: PS00204; FERRITIN_2; 1.
DR PROSITE: PS00905; FERRITIN_LIKE; 1.
SQ SEQUENCE 170 AA; 19536 MW; E229F11EBCD10FD4 CRC64;

Query Match 96.8%; Score 30; DB 5; Length 170;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
Db 71 IORGR 76

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Search completed: April 15, 2004, 10:30:48
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 10:27:10 ; Search time 55 Seconds
(without alignments)
30.823 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31
Sequence: 1 VQRGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
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4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 31 | 100.0 | 148 | AAU19794 | Aau19794 Human nov |
| 4 | 31 | 100.0 | 148 | ABP47854 | Abp47854 Human pol |
| 5 | 31 | 100.0 | 148 | ABP48014 | Abp48014 Human pol |
| 6 | 31 | 100.0 | 148 | ADC10816 | Adc10816 Human ext |
| 7 | 31 | 100.0 | 148 | ADC10976 | Adc10976 Human pro |
| 8 | 31 | 100.0 | 169 | AAE36077 | Aae36077 Flax Conl |
| 9 | 31 | 100.0 | 192 | AAE33535 | Aae33535 Rat-human |
| 10 | 31 | 100.0 | 192 | AAE33537 | Aae33537 Human alp |
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| 12 | 31 | 100.0 | 195 | AAU76860 | Aau76860 Human int |
| 13 | 31 | 100.0 | 206 | ABG29235 | Abg29235 Novel hum |
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| 15 | 31 | 100.0 | 214 | AAE33540 | Aae33540 Human alp |
| 16 | 31 | 100.0 | 378 | AAU47587 | Aau47587 Propionib |
| 17 | 31 | 100.0 | 378 | ABM44106 | Abm44106 Propionib |
| 18 | 31 | 100.0 | 755 | AAU57634 | Aau57634 Propionib |
| 19 | 31 | 100.0 | 755 | ABMS4153 | Abms4153 Propionib |
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| 21 | 31 | 100.0 | 1179 | ABD90759 | Abd90759 Human tum |
| 22 | 31 | 100.0 | 1179 | ABP64915 | Abp64915 Human pro |
| 23 | 31 | 100.0 | 1179 | ABU54466 | Abu54466 Human tum |
| 24 | 31 | 100.0 | 1183 | AAU07728 | Aau07728 Armenian |
| 25 | 30 | 96.8 | 35 | AAR87641 | Aar87641 Synthetic |

ALIGNMENTS

RESULT 1

AAB50043
ID AAB50043 standard; peptide; 6 AA.

XX
AC AAB50043;

DT 14-MAR-2001 (first entry)

DE Human alpha1 integrin domain epitope.

XX Human; alpha1 integrin domain; alpha1beta1 function blocking antibody;
KW inflammatory disorder; rheumatoid arthritis; skin condition; asthma;
KW bronchitis; headache; antipyretic; fever; gastrointestinal;
KW vascular disease; autoimmune; respiratory distress syndrome;
KW endotoxin shock syndrome; atherosclerosis.

XX Homo sapiens.

XX WO2000072881-A1.

XX 07-DEC-2000.

XX 01-JUN-2000; 2000WO-US015004.

XX 01-JUN-1999; 99US-0137038P.

XX 29-FEB-2000; 2000US-0185336P.

XX (BIOJ) BIOGEN INC.

XX De Fougereolles A, Gotwals P, Lobb R, Koteliensky V;

XX WPI; 2001-061448/07.

XX Use of blocking monoclonal antibody capable of binding to an epitope of
VLA-1 for treating inflammatory disorders, in particular arthritis.

XX Claim 1; Fig 15; 60pp; English.

XX The present invention relates to the use of an alpha1beta1 function
blocking antibody capable of binding the present epitope of human alpha1
integrin domain (VLA-1). The antibody of the present invention is useful
for treating an inflammatory disorder e.g. rheumatoid arthritis, skin
CC related conditions such as psoriasis, eczema, burns and dermatitis,
CC asthma, bronchitis, menstrual cramps, tendinitis, bursitis, and the
CC treatment of pain and headaches, or as an antipyretic, for the treatment
CC of fever, gastrointestinal conditions such as inflammatory bowel
CC diseases, Crohn's disease, gastritis and vascular diseases, migraine
CC headaches, periarthritis nodosa, thyroiditis, aplastic anaemia, Hodgkin's

CC disease, rheumatic fever, type I diabetes, myasthenia gravis, multiple
CC sclerosis, sarcoidosis, nephrotic syndrome, myocardial ischaemia,
CC allergic rhinitis, respiratory distress syndrome, endotoxin shock
CC syndrome and atherosclerosis
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQRCGR 6
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Db 1 VQRCGR 6

RESULT 2

AAU19634
ID AAU19634 standard; protein; 148 AA.

XX
AC AAU19634;

XX
DT 04-DEC-2001 (first entry)

XX
DE Human novel extracellular matrix protein, Seq ID No 284.

XX Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV;
KW antineuritic; antirheumatic; antisclerotic; cardiac; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
KW antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancers; hyperproliferative disorder; breast neoplasm; melanoma;
KW Searcy syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW cardiac arrest; tachycardia; angina; infection; corneal infections;
KW wound healing; immunogen; gene therapy; antisense; food additive.

XX Homo sapiens.

XX WO200155368-A1.

XX
PD 02-AUG-2001.

XX
FF 17-JAN-2001; 2001WO-US001348.

XX
PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209457P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

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PR 11-JUL-2000; 2000US-0217487P.

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PR 14-JUL-2000; 2000US-0218230P.

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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-465572/50.
 DR N-PSDB; AAS31365.
 XX
 PT Nucleic acid molecules encoding human secreted extracellular matrix
 PT proteins, used in preventing, treating or ameliorating a disorder, e.g.
 PT Alzheimer's and Parkinson's diseases and cancers.
 XX
 PS Claim 11; SEQ ID NO 444; 577bp; English.
 XX
 CC The invention relates to isolated nucleic acid molecules encoding novel
 CC human secreted extracellular matrix proteins (SPs). The polynucleotides
 CC and proteins are used to prevent, treat a medical condition in e.g.
 CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For
 CC example, disorders associated with decreased expression of SPs. The SP
 CC polynucleotide or a vector expressing them may be administered to treat
 CC diseases by gene therapy. Antisense molecules may be administered to down
 CC regulate expression of SPs by binding with the cells own genes and
 CC preventing their expression. The polynucleotides may also be used as DNA
 CC probes in diagnostic assays. The SPs may also be used as antigens to
 CC produce antibodies and to identify modulators (agonists and antagonists)
 CC of the SPs. The anti-(SP) antibodies and antagonists may also be used to
 CC down regulate expression and activity of SP and as diagnostic agents for
 CC detecting the presence of SPs in samples. The disorders include for
 CC example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency
 CC virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis),
 CC cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of
 CC the breast or liver, Sezary syndrome and Gaucher's disease), neurological
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-
 CC /cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina),
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC (e.g. corneal infections). Other uses include wound healing, maintenance
 CC of organs before transplantation, support of cell culture of primary

Query Match 100.0%; Score 31; DB 4; Length 148;
 Best Local Similarity 100.0%; Pred. No. 2.le+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGG 6
 DB 116 VORGG 121

```

RESULT 4
ID ABP47854 standard; protein; 148 AA.
XX AC ABP47854;
XX DT 23-AUG-2002 (first entry)
XX DE Human polypeptide SEQ ID NO 284.
XX KW Human; neutrotropic; neuroprotective; cytostatic; dermatological; virucide;
XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN US2002042386-A1.
XX PD 11-APR-2002.
XX PF 17-JAN-2001; 2001US-00764870.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 11-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
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XX PR 01-SEP-2000; 2000US-0229344P.
XX PR 05-SEP-2000; 2000US-0229345P.
XX PR 05-SEP-2000; 2000US-0229509P.
XX PR 08-SEP-2000; 2000US-0229513P.
XX PR 21-SEP-2000; 2000US-0231413P.
XX PR 21-SEP-2000; 2000US-0234223P.
XX PR 25-SEP-2000; 2000US-0234274P.
XX PR 27-SEP-2000; 2000US-0234997P.
XX PR 29-SEP-2000; 2000US-0236327P.
XX PR 29-SEP-2000; 2000US-0236367P.
XX PR 29-SEP-2000; 2000US-0236368P.
XX PR 29-SEP-2000; 2000US-0236369P.
XX PR 29-SEP-2000; 2000US-0236370P.
XX PR 02-OCT-2000; 2000US-0236802P.
XX PR 02-OCT-2000; 2000US-0237037P.
XX PR 02-OCT-2000; 2000US-0237038P.
XX PR 02-OCT-2000; 2000US-0237039P.
XX PR 02-OCT-2000; 2000US-0237040P.
XX PR 13-OCT-2000; 2000US-0239935P.
XX PR 20-OCT-2000; 2000US-0240960P.
XX PR 20-OCT-2000; 2000US-0241785P.
XX PR 20-OCT-2000; 2000US-0241809P.

PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX PI Rosen CA, Ruben SM, Barash SC;
XX WI 2002-470713/50.
XX DR N-PSDB; ABQ66529.
XX PT New nucleic acid encoding human proteins, useful for diagnosis, treatment
XX PT and prevention of e.g. osteoporosis, also related polypeptides and
XX PT antibodies.
XX PS Claim 11; SEQ ID NO 284; 235pp + Sequence Listing; English.
XX CC The invention relates to novel Genes (ABQ66521-ABQ66785) and proteins
XX CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating
XX CC medical conditions e.g. by protein or gene therapy. The genes are
XX CC isolated from a range of human tissues disclosed in the specification.
XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX CC disorders e.g. Addison's disease, allergies, diabetes mellitus, Crohn's disease,
XX CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
XX CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX CC infectious diseases such as viral, bacterial, fungal and parasitic
XX CC infections. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html?docID=999999764870
XX SQ Sequence 148 AA;
Query Match 100.0%; Score 31; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VORGER 6
Db 116 VORGER 121
RESULT 5
ID ABP48014 standard; protein; 148 AA.
XX AC ABP48014;
XX DT 23-AUG-2002 (first entry)
XX DE Human polypeptide SEQ ID NO 444.
XX KW Human; neutrotropic; neuroprotective; cytostatic; dermatological; virucide;
XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN US2002042386-A1.
XX PD 11-APR-2002.

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XX 17-JAN-2001; 2001US-00764870.
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216847P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
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 PR 21-SEP-2000; 2000US-0231427P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
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 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR (ROSE/) ROSEN C A.
 PR (RUBE/) RUBEN S M.
 PR (BARA/) BARASH S C.
 PI Rosen CA, Ruben SM, Barash SC;
 DR WPI; 2002-470713/50.
 DR N-PSDB; ABQ65689.
 XX
 PT New nucleic acid encoding human proteins, useful for diagnosis, treatment
 PT and prevention of e.g. osteoporosis, also related polypeptides and
 PT antibodies.
 XX
 PS Claim 11; SEQ ID NO 44; 235pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABQ6521-ABQ66785) and proteins
 CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.

CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html?DocID=999909764870
 XX
 SQ Sequence 148 AA;
 Query Match 100.0%; Score 31; DB 5; Length 148;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQGGG 6
 Db 116 VQGGG 121
 RESULT 6
 ADC10816
 ID ADC10816 standard; protein; 148 AA.
 XX
 AC ADC10816;
 XX
 DT 18-DEC-2003 (first entry)
 DE Human extracellular matrix protein from gene 9.
 XX
 KW Extracellular matrix protein; cytostatic; antibacterial; virucide;
 KW neuroprotective; gynaecological; gastrointestinal-gen; cardiant;
 KW cardiovascular-gen; nephrotropic; antiinflammatory; muscular-gen;
 KW respiratory-gen; immunosuppressive; cerebroprotective; vasotropic;
 KW neotropic; antiallergic; cancer; bacterial infection; viral infection;
 KW neural disorder; immune system disorder; blood disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW inflammatory disorder; proliferative disorder; Human.
 OS Homo sapiens.
 XX
 XX US2003059875-A1.
 PN
 PD 27-MAR-2003.
 XX
 XX 19-APR-2002; 2002US-00125540.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
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PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
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PR 01-NOV-2000; 2000US-0244617P.
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PR 08-NOV-2000; 2000US-0246476P.
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PR 08-NOV-2000; 2000US-0246523P.
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PR 08-NOV-2000; 2000US-0246609P.
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PR 17-NOV-2000; 2000US-0249215P.
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PR 17-NOV-2000; 2000US-0249245P.
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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 05-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764870.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM, Barash SC;
WPI; 2003-743765/70.
N-PSDE; ADC10551.
New isolated nucleic acids and polypeptides, useful for diagnosing, treating, and/or preventing disorders, such as cancer, infections, cardiovascular and inflammatory diseases.
Claim 11; SEQ ID NO 284; 235pp; English.
The invention relates to an isolated nucleic acid molecule (cDNA) encoding a human extracellular matrix protein, representing one of 161 novel genes. Also included are recombinant vectors, host cells (expressing the protein), the extracellular matrix proteins (including their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition (comprising determining the presence or absence of a mutation in the nucleic acid and diagnosing a condition based on the presence or absence of the mutation), diagnosing a pathological condition or susceptibility to a pathological condition (comprising determining the presence or amount of expression of the protein in a biological sample and diagnosing a condition based on the presence or amount of expression of the protein), preventing, treating or ameliorating a medical condition by administering the nucleic acid or protein to a mammalian subject, identifying a binding partner to the

CC protein, the gene corresponding to the cDNA sequence, and identifying an
 CC activity in a biological assay (comprising expressing the nucleic acid in
 CC a cell, isolating the supernatant, detecting an activity in a biological
 CC assay and identifying the protein in the supernatant having the
 CC activity). The nucleic acids and proteins display the following
 CC activities: Cytostatic, antibacterial, Virucide, Neuroprotective,
 CC Gynaecological, Gastrointestinal-Gen, Cardiant, Cardiovascular-Gen,
 CC Nephrotropic, Antiinflammatory, Muscular-Gen, Respiratory-Gen,

Query Match 100.0%; Score 31; DB 7; Length 148;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6
 DB 116 VORGR 121

RESULT 7

ADC10976
 ID ADC10976 standard; protein; 148 AA.

XX AC ADC10976;

XX DT 18-DEC-2003 (first entry)

XX DE Human protein from extracellular matrix gene 9 #2

XX KW Extracellular matrix protein; cytostatic; antibacterial; virucide;
 KW neuroprotective; gynaecological; gastrointestinal-Gen; cardiant;
 KW cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen;
 KW respiratory-Gen; immunosuppressive; cerebrotective; vasotropic;
 KW neotropic; antiallergic; cancer; bacterial infection; viral infection;
 KW neural disorder; immune system disorder; blood disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW inflammatory disorder; proliferative disorder; Human.

XX OS Homo sapiens.

XX PN US2003059875-A1.

XX PD 27-MAR-2003.

XX PF 19-APR-2002; 2002US-00125540.

XX PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184684P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209457P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

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PR 14-AUG-2000; 2000US-0224518P.

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 PR 21-SEP-2000; 2000US-0234274P.
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 PR 29-SEP-2000; 2000US-0236367P.
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 PR 13-OCT-2000; 2000US-0239935P.
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 PR 08-NOV-2000; 2000US-0245474P.
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| XX | SQ | Sequence 192 AA; |
| | | Query Match 100.0%; Score 31; DB 6; Length 192; |
| | | Best Local Similarity 100.0%; Pred. No. 2.7e+02; |
| | | Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | | 1 VQRGGR 6 |
| | | |
| Dd | | 73 VQRGGR 78 |
| RESULT 10 | | |
| AAE33537 | | |
| ID | AAE33537 standard; protein; 192 AA. | |
| XX | AC | AAE33537; |
| XX | AC | XX |
| XX | DT | 02-APR-2003 (first entry) |
| XX | DE | Human alpha 1-I domain protein #1. |
| XX | KW | Human; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anemia; periarthritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; alpha 1-I protein. |
| XX | OS | Homo sapiens. |
| XX | PN | WO200283854-A2. |
| PD | PD | 24-OCT-2002. |
| PF | PF | 12-APR-2002; 2002WO-US011521. |
| PR | PR | 13-APR-2001; 2001US-0283794P. |
| PR | PR | 06-JUL-2001; 2001US-0303689P. |
| XX | PA | (BIOJ) BIOGEN INC. |
| PA | PI | Lynne PD, Garber EA, Saldanha JW, Karpusas M; |
| XX | DR | WPI; 2003-093009/08. |
| PT | PT | New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells or fibrosis. |
| PS | PS | Example 24; Page 94; 248pp; English. |
| XX | CC | The present invention relates to novel antibodies that specifically bind to vary late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders such as skin related conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal proliferation of hair follicle cells), fibrosis (e.g. kidney or lung fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease, gastritis, irritable bowel syndrome, colitis and colorectal cancer), vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia, periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, Crohn's disease. |

CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC human I-I domain protein. This sequence is used in the exemplification of
 CC the invention

XX Sequence 192 AA;

Query Match 100.0%; Score 31; DB 6; Length 192;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRGGR 6

Db 73 VQRGGR 78

RESULT 11

AAU76851
 ID AAU76851 standard; protein; 195 AA.

XX AC AAU76851;

XX DT 21-MAY-2002 (first entry)

XX DE Human integrin alpha subunit Alpha 1 (CD49a) A domain.

XX KW Human; integrin alpha subunit; A domain; CD49a; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; Alpha 1;
 KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.

XX OS Homo sapiens.

XX PN WO200209737-A1.

XX PD 07-FEB-2002.

XX PF 31-JUL-2001; 2001WO-US023957.

XX PR 31-JUL-2000; 2000US-0221950P.

XX PR 11-JAN-2001; 2001US-00758493.

XX PR 13-MAR-2001; 2001US-00805354.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Arnaout AM, Li R, Xiong J;

XX DR WPI; 2002-188687/24.

XX PT Novel high affinity integrin polypeptide useful for treating restenosis

PT and parasitic diseases, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.

PS Example 2; Fig 5; 55pp; English.

XX CC The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in

CC two-hybrid or three-hybrid assays. This sequence represents the human
 CC integrin alpha subunit Alpha 1 (CD49a) A domain

XX Sequence 195 AA;

Query Match 100.0%; Score 31; DB 5; Length 195;

Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQRGGR 6

Db 75 VQRGGR 80

RESULT 12

AAU76860
 ID AAU76860 standard; protein; 195 AA.

XX AC AAU76860;

XX DT 21-MAY-2002 (first entry)

XX DE Human integrin alpha subunit Alpha 1 (CD49a) variant A domain.

XX KW Human; integrin alpha subunit; A domain; CD49a; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
 KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
 KW mutein; Alpha 1.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 193

FT FT /note= "wild-type Ile substituted by any other amino acid"

XX PN WO200209737-A1.

XX PD 07-FEB-2002.

XX PF 31-JUL-2001; 2001WO-US023957.

XX PR 31-JUL-2000; 2000US-0221950P.

XX PR 11-JAN-2001; 2001US-00758493.

XX PR 13-MAR-2001; 2001US-00805354.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Arnaout AM, Li R, Xiong J;

XX DR WPI; 2002-188687/24.

XX PT Novel high affinity integrin polypeptide useful for treating restenosis

PT and parasitic diseases, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.

PS Claim 45; Page; 55pp; English.

XX CC The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in

CC two-hybrid or three-hybrid assays. This sequence represents a human
 CC integrin alpha subunit Alpha 1 (CD49a) variant A domain. Note: This
 CC variant sequence is not featured in the specification but has been
 CC derived from the wild-type protein shown in AAU75851
 XX
 SQ Sequence 195 AA;
 Query Match 100.0%; Score 31; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQRGR 6
 |||||
 Db 75 VQRGR 80

RESULT 13
 ABG29235
 ID ABG29235 standard; protein; 206 AA.
 XX AC ABG29235;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #29226.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX WO200175067-A2.
 XX FN 11-OCT-2001.
 XX PD 30-MAR-2001; 2001WO-US008631.
 XX PF 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX PA Drmanac RT, Liu C, Tang YT;
 XX PI WPI; 2001-639362/73.
 XX DR N-PSDB; AAS93422.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 59594; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 31; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQRGR 6
 |||||
 Db 101 VQRGR 106

RESULT 14
 AAB50042
 ID AAB50042 standard; protein; 214 AA.
 XX AC AAB50042;
 XX DT 14-MAR-2001 (first entry)
 XX DE Human alpha integrin domain.
 XX Human; alpha integrin domain; alfa1beta1 function blocking antibody;
 KW inflammatory disorder; rheumatoid arthritis; skin condition; asthma;
 KW bronchitis; headache; antipyretic; fever; gastrointestinal;
 KW vascular disease; autoimmune; respiratory distress syndrome;
 KW endotoxin shock syndrome; atherosclerosis.
 XX OS Homo sapiens.
 XX WO200072881-A1.
 XX FN 07-DEC-2000.
 XX PD 01-JUN-2000; 2000WO-US015004.
 XX PF 01-JUN-1999; 99US-0137038P.
 XX PR 29-FEB-2000; 2000US-0185336P.
 XX (BIOJ) BIOGEN INC.
 XX PI De Fougereolles A, Gotwals P, Lobb R, Koteliensky V;
 XX WPI; 2001-061448/07.
 XX Use of blocking monoclonal antibody capable of binding to an epitope of
 PT VLA-1 for treating inflammatory disorders, in particular arthritis.
 XX Example 14; Fig 15; 60pp; English.

CC The present invention relates to the use of an alpha1beta1 function
 CC blocking antibody capable of binding an epitope of human alpha integrin
 CC domain (VLA-1; see AAB50043). The antibody of the present invention is
 CC useful for treating an inflammatory disorder e.g. rheumatoid arthritis,
 CC skin related conditions such as psoriasis, eczema, burns and dermatitis,
 CC asthma, bronchitis, menstrual cramps, tendonitis, bursitis, and the
 CC treatment of pain and headaches, or as an antipyretic, for the treatment
 CC of fever, gastrointestinal conditions such as inflammatory bowel
 CC diseases, Crohn's disease, gastritis and vascular diseases, migraine
 CC headaches, periarthritis nodosa, thyroiditis, aplastic anaemia, Hodgkin's
 CC disease, rheumatic fever, type I diabetes, myasthenia gravis, multiple
 CC sclerosis, sarcoidosis, nephrotic syndrome, myocardial ischaemia,
 CC allergic rhinitis, respiratory distress syndrome, endotoxin shock
 CC syndrome and atherosclerosis. The present sequence is the human alpha
 CC integrin domain
 XX Sequence 214 AA;
 Query Match 100.0%; Score 31; DB 4; Length 214;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGG 6
 DB 91 VORGG 96

RESULT 15

AAE33540
 ID AAE33540 standard; protein; 214 AA.

AC AAE33540;

DT 02-APR-2003 (first entry)

DE Human alpha 1-I domain protein #2.

Human; very late activation antigen; VLA-1; beta1 containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; alpha 1-I protein.

OS Homo sapiens.

FN WO200283854-A2.

PD 24-OCT-2002.

PF 12-APR-2002; 2002WO-US011521.

PR 13-APR-2001; 2001US-0283794P.

PR 06-JUL-2001; 2001US-0303689P.

PA (BIOJ) BIOGEN INC.

PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;

DR WPI; 2003-093009/08.

New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells or fibrosis.

Example 18; Fig 12; 248pp; English.

The present invention relates to novel antibodies that specifically bind to very late activation (VLA-1; beta1 containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders such as skin related conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal proliferation of hair follicle cells), fibrosis (e.g. kidney or lung fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, bronchitis, tendonitis, bursitis, fever, migraine headaches, gastrointestinal conditions (e.g. inflammatory bowel disease, Crohn's disease, gastritis, irritable bowel syndrome, colitis and colorectal cancer), vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia, periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid arthritis, systemic lupus erythematosus and multiple sclerosis), renal failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis, polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or immediate hypersensitivity), graft and transplant rejections, graft versus host disease, conjunctivitis, swelling occurring after injury.

CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is human 1-I domain protein. This sequence is used in the exemplification of the invention

SQ Sequence 214 AA;

Query Match 100.0%; Score 31; DB 6; Length 214;
 Best Local Similarity 100.0%; Pred. No. 3e+02; 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 VORGG 6
 DB 91 VORGG 96

Search completed: April 15, 2004, 10:28:22
 Job time : 57 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2004, 10:29:26 ; Search time 42 Seconds
(without alignments)
39.382 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31

Sequence: 1 VORGR 6

Scoring table: BIOSUM62

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Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 31 | 100.0 | 6 | 9 | US-09-996-738-9 |
| 3 | 31 | 100.0 | 6 | 12 | US-10-625-260-8 |
| 4 | 31 | 100.0 | 6 | 13 | US-10-061-658-8 |
| 5 | 31 | 100.0 | 7 | 12 | US-10-625-260-10 |
| 6 | 31 | 100.0 | 7 | 13 | US-10-061-658-10 |
| 7 | 31 | 100.0 | 148 | 9 | US-09-764-870-284 |
| 8 | 31 | 100.0 | 148 | 9 | US-09-764-870-444 |
| 9 | 31 | 100.0 | 148 | 14 | US-10-125-540-284 |
| 10 | 31 | 100.0 | 148 | 14 | US-10-125-540-444 |
| 11 | 31 | 100.0 | 169 | 14 | US-10-165-289A-4 |
| 12 | 31 | 100.0 | 192 | 12 | US-10-346-863-57 |
| 13 | 31 | 100.0 | 195 | 10 | US-09-805-354-5 |
| 14 | 31 | 100.0 | 195 | 14 | US-10-144-259-5 |
| 15 | 31 | 100.0 | 212 | 9 | US-09-996-738-6 |

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16 31 100.0 214 12 US-10-625-260-6 Sequence 6, Appli
17 31 100.0 214 12 US-10-625-260-9 Sequence 9, Appli
18 31 100.0 214 13 US-10-061-658-6 Sequence 6, Appli
19 31 100.0 214 13 US-10-061-658-9 Sequence 9, Appli
20 31 100.0 223 15 US-10-369-433-14140 Sequence 14140, A
21 31 100.0 394 15 US-10-369-493-15276 Sequence 15276, A
22 31 100.0 395 15 US-10-369-493-11657 Sequence 11657, A
23 31 100.0 395 15 US-10-369-493-14549 Sequence 14549, A
24 31 100.0 395 15 US-10-369-493-15117 Sequence 15117, A
25 31 100.0 526 12 US-10-425-114-60850 Sequence 60850, A
26 31 100.0 1151 10 US-09-984-130-103 Sequence 103, App
27 31 100.0 1151 10 US-09-836-332A-103 Sequence 103, App
28 31 100.0 1179 12 US-09-918-715-250 Sequence 250, App
29 30 96.8 196 12 US-10-424-599-251702 Sequence 251702,
30 30 96.8 269 13 US-10-027-806-24 Sequence 24, Appl
31 30 96.8 269 13 US-10-034-623-24 Sequence 24, Appl
32 30 96.8 269 14 US-10-037-801-24 Sequence 24, Appl
33 30 96.8 269 14 US-10-029-120-24 Sequence 24, Appl
34 30 96.8 273 13 US-10-037-806-56 Sequence 56, Appl
35 30 96.8 273 13 US-10-034-623-56 Sequence 56, Appl
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37 30 96.8 273 14 US-10-029-120-56 Sequence 56, Appl
38 28 90.3 70 12 US-10-424-599-164464 Sequence 164464,
39 28 90.3 117 12 US-10-424-599-282180 Sequence 282180,
40 28 90.3 136 9 US-09-894-998-40 Sequence 40, Appl
41 28 90.3 136 14 US-10-121-388-40 Sequence 40, Appl
42 28 90.3 136 14 US-10-200-562-40 Sequence 40, Appl
43 28 90.3 136 14 US-10-237-551-40 Sequence 40, Appl
44 28 90.3 141 12 US-10-424-599-275717 Sequence 275717,
45 28 90.3 168 14 US-10-165-289A-2 Sequence 2, Appli

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ALIGNMENTS

RESULT 1

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US-09-996-738-8
; Sequence 8, Application US/09996738
; Patent No. US20020146417A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: De Fougereolles, Antonin
; APPLICANT: Gotwals, Philip
; APPLICANT: Lobb, Roy
; APPLICANT: Kotliansky, Victor
; TITLE OF INVENTION: Method for the Treatment of Inflammatory
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: A076PCT
; CURRENT APPLICATION NUMBER: US/09/996,738
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/185336
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/137038
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-996-738-8

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Query Match 100.0%; Score 31; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6

Db 1 VORGR 6

RESULT 2

US-09-996-738-9

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; Sequence 9, Application US/09996738
; Patent No. US20020146417A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: De Fougereolles, Antonin
; APPLICANT: Gotwals, Philip
; APPLICANT: Lobb, Roy
; APPLICANT: Koteliarsky, Victor
; TITLE OF INVENTION: Method for the Treatment of Inflammatory
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: A076PCT
; CURRENT APPLICATION NUMBER: US/09/996,738
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/185336
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/137038
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-996-738-9

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Query Match      100.0%; Score 31; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VORGGG 6
Db      1 VORGGG 6

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RESULT 3

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; Sequence 8, Application US/10625260
; Publication No. US20040037827A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Gotwals, Philip
; APPLICANT: Koteliarsky, Victor
; TITLE OF INVENTION: Method for the Treatment of Fibrosis
; FILE REFERENCE: A073US
; CURRENT APPLICATION NUMBER: US/10/625,260
; CURRENT FILING DATE: 2003-07-22
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/137,214
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-625-260-8

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Query Match      100.0%; Score 31; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VORGGG 6
Db      1 VORGGG 6

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RESULT 4

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US-10-061-658-8
; Sequence 8, Application US/10061658
; Publication No. US20020182213A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.

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; APPLICANT: Gotwals, Philip
; APPLICANT: Koteliarsky, Victor
; TITLE OF INVENTION: Method for the Treatment of Fibrosis
; FILE REFERENCE: A073US
; CURRENT APPLICATION NUMBER: US/10/061,658
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/137,214
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/130,847
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-061-658-8

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Query Match      100.0%; Score 31; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VORGGG 6
Db      1 VORGGG 6

```

RESULT 5

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US-10-625-260-10
; Sequence 10, Application US/10625260
; Publication No. US20040037827A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Gotwals, Philip
; APPLICANT: Koteliarsky, Victor
; TITLE OF INVENTION: Method for the Treatment of Fibrosis
; FILE REFERENCE: A073US
; CURRENT APPLICATION NUMBER: US/10/625,260
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: 60/137,214
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/130,847
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-10-625-260-10

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```

Query Match      100.0%; Score 31; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VORGGG 6
Db      1 VORGGG 6

```

RESULT 6

```

US-10-061-658-10
; Sequence 10, Application US/10061658
; Publication No. US20020182213A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Gotwals, Philip
; APPLICANT: Koteliarsky, Victor
; TITLE OF INVENTION: Method for the Treatment of Fibrosis
; FILE REFERENCE: A073US
; CURRENT APPLICATION NUMBER: US/10/061,658
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/137,214

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; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/130,847
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-10-061-658-10

Query Match
  100.0%; Score 31; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGRGR 6
Db 1 VQGRGR 6

RESULT 7
US-09-764-870-284
; Sequence 284, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-284

Query Match
  100.0%; Score 31; DB 9; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGRGR 6
Db 116 VQGRGR 121

RESULT 8
US-09-764-870-444
; Sequence 444, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 444
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-444

Query Match
  100.0%; Score 31; DB 9; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGRGR 6
Db 116 VQGRGR 121

RESULT 9
US-10-125-540-284
; Sequence 284, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-284

Query Match
  100.0%; Score 31; DB 14; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGRGR 6
Db 116 VQGRGR 121

RESULT 10
US-10-125-540-444
; Sequence 444, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 444
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-444

Query Match
  100.0%; Score 31; DB 14; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGRGR 6
Db 116 VQGRGR 121

RESULT 11
US-10-155-289A-4
; Sequence 4, Application US/1015289A
; Publication No. US20030159174A1
; GENERAL INFORMATION:
; APPLICANT: QIU, Xiao
; APPLICANT: TRUSKA, Martin
; APPLICANT: HU, Zhiyuan
; TITLE OF INVENTION: Plax (Linum usitatissimum L.)
; TITLE OF INVENTION: Seed-Specific Promoters
; FILE REFERENCE: ENZ-005
; CURRENT APPLICATION NUMBER: US/10/155,289A
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/295823
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; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Linum usitatissimum
US-10-165-289A-4

Query Match      100.0%; Score 31; DB 14; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGGGR 6
Db 72 VORGGGR 77

RESULT 12
US-10-346-863-57
; Sequence 57, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-57

Query Match      100.0%; Score 31; DB 12; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGGGR 6
Db 74 VORGGGR 79

RESULT 13
US-09-805-354-5
; Sequence 5, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-5

Query Match      100.0%; Score 31; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGGGR 6
Db 75 VORGGGR 80

RESULT 14
US-10-144-259-5
; Sequence 5, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-5

Query Match      100.0%; Score 31; DB 14; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGGGR 6
Db 75 VORGGGR 80

RESULT 15
US-09-996-738-6
; Sequence 6, Application US/09996738
; Patent No. US20020146417A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: De Fougereolles, Antonin
; APPLICANT: Gotwals, Philip
; APPLICANT: Lobb, Roy
; APPLICANT: Kotliansky, Victor
; TITLE OF INVENTION: Method for the Treatment of Inflammatory
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: A076PCT
; CURRENT APPLICATION NUMBER: US/09/996,738
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/185336
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/137038
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-996-738-6
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Query Match 100.0%; Score 31; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGGG 6
| | | | |
Db 91 VQGGG 96

Search completed: April 15, 2004, 10:35:25
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2004, 10:27:11 ; Search time 23 Seconds
(without alignments)
13.468 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31

Sequence: 1 VQRGR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/Backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|----------------------|
| 1 | 31 | 100.0 | 6 | 4 | US-10-061-658-8 |
| 2 | 31 | 100.0 | 7 | 4 | US-10-061-658-10 |
| 3 | 31 | 100.0 | 173 | 4 | US-09-252-991A-25437 |
| 4 | 31 | 100.0 | 214 | 4 | US-10-061-658-6 |
| 5 | 31 | 100.0 | 214 | 4 | US-10-061-658-9 |
| 6 | 31 | 100.0 | 296 | 4 | US-09-252-991A-32247 |
| 7 | 31 | 100.0 | 331 | 4 | US-09-252-991A-24420 |
| 8 | 31 | 100.0 | 348 | 4 | US-09-489-039A-10294 |
| 9 | 31 | 100.0 | 391 | 4 | US-09-252-991A-27211 |
| 10 | 31 | 100.0 | 863 | 4 | US-09-252-991A-26099 |
| 11 | 31 | 100.0 | 877 | 4 | US-09-252-991A-25547 |
| 12 | 31 | 100.0 | 1011 | 4 | US-09-252-991A-32419 |
| 13 | 30 | 96.8 | 35 | 3 | US-08-750-624-3 |
| 14 | 30 | 96.8 | 269 | 4 | US-09-408-020-24 |
| 15 | 30 | 96.8 | 273 | 4 | US-09-408-020-56 |
| 16 | 30 | 96.8 | 431 | 4 | US-09-543-681A-7623 |
| 17 | 28 | 90.3 | 136 | 4 | US-09-894-998A-40 |
| 18 | 28 | 90.3 | 211 | 4 | US-09-252-991A-26756 |
| 19 | 28 | 90.3 | 243 | 4 | US-09-252-991A-28884 |
| 20 | 28 | 90.3 | 263 | 4 | US-09-252-991A-27793 |
| 21 | 28 | 90.3 | 321 | 4 | US-09-252-991A-30008 |
| 22 | 28 | 90.3 | 325 | 4 | US-09-252-991A-25406 |
| 23 | 28 | 90.3 | 376 | 4 | US-09-894-998A-39 |
| 24 | 28 | 90.3 | 417 | 4 | US-09-489-039A-11555 |
| 25 | 28 | 90.3 | 422 | 4 | US-09-252-991A-19232 |
| 26 | 28 | 90.3 | 443 | 4 | US-09-252-991A-21256 |
| 27 | 28 | 90.3 | 464 | 4 | US-09-252-991A-26212 |

Sequence 18961, A
Sequence 2, Appli
Sequence 25655, A
Sequence 25082, A
Sequence 24072, A
Sequence 19603, A
Sequence 32311, A
Sequence 27880, A
Sequence 20370, A
Sequence 17227, A
Sequence 29554, A
Sequence 1118, A
Sequence 30138, A
Sequence 11, Appl
Sequence 18172, A
Sequence 22993, A
Sequence 26085, A
Sequence 30609, A

ALIGNMENTS

RESULT 1

US-10-061-658-8
; Sequence 8, Application US/10061658
; Patent No. 6652856
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Gotwals, Philip
; APPLICANT: Koteliansky, Victor
; TITLE OF INVENTION: Method for the Treatment of Fibrosis
; FILE REFERENCE: A073US
; CURRENT APPLICATION NUMBER: US/10/061,658
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/137,214
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/130,847
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-061-658-8

Query Match 100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VQRGR 6
| | | | |
Db 1 VQRGR 6

RESULT 2

US-10-061-658-10
; Sequence 10, Application US/10061658
; Patent No. 6652856
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Gotwals, Philip
; APPLICANT: Koteliansky, Victor
; TITLE OF INVENTION: Method for the Treatment of Fibrosis
; FILE REFERENCE: A073US
; CURRENT APPLICATION NUMBER: US/10/061,658
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/137,214
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/130,847
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 7

; TYPE: PRT

; ORGANISM: homo sapien

US-10-061-658-10

Query Match 100.0%; Score 31; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6

Db 1 VORGR 6

RESULT 3

US-09-252-991A-25437

; Sequence 25437, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: A073US

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 25437

; LENGTH: 173

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25437

Query Match 100.0%; Score 31; DB 4; Length 173;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORGR 6

Db 59 VORGR 64

RESULT 4

US-10-061-658-6

; Sequence 6, Application US/10061658

; Patent No. 6652856

; GENERAL INFORMATION:

; APPLICANT: Biogen, Inc.

; APPLICANT: Gotwals, Philip

; APPLICANT: Koteliansky, Victor

; TITLE OF INVENTION: Method for the Treatment of Fibrosis

; FILE REFERENCE: A073US

; CURRENT APPLICATION NUMBER: US/10/061,658

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/137,214

; PRIOR FILING DATE: 1999-06-01

; PRIOR APPLICATION NUMBER: 60/130,847

; PRIOR FILING DATE: 1999-04-22

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-061-658-6

Query Match

Best Local Similarity 100.0%; Score 31; DB 4; Length 214;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 VORGR 6

Db

91 VORGR 96

RESULT 5

US-10-061-658-9

; Sequence 9, Application US/10061658

; Patent No. 6652856

; GENERAL INFORMATION:

; APPLICANT: Biogen, Inc.

; APPLICANT: Gotwals, Philip

; APPLICANT: Koteliansky, Victor

; TITLE OF INVENTION: Method for the Treatment of Fibrosis

; FILE REFERENCE: A073US

; CURRENT APPLICATION NUMBER: US/10/061,658

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/137,214

; PRIOR FILING DATE: 1999-06-01

; PRIOR APPLICATION NUMBER: 60/130,847

; PRIOR FILING DATE: 1999-04-22

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-061-658-9

Query Match

Best Local Similarity 100.0%; Score 31; DB 4; Length 214;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 VORGR 6

Db

91 VORGR 96

RESULT 6

US-09-252-991A-32247

; Sequence 32247, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 32247

; LENGTH: 296

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32247

Query Match

Best Local Similarity 100.0%; Score 31; DB 4; Length 296;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 VORGR 6

Db

73 VORGR 78

RESULT 7

US-09-252-991A-24420

; Sequence 24420, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24420
 ; LENGTH: 331
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24420

Query Match 100.0%; Score 31; DB 4; Length 331;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VORGR 6
 Db 110 VORGR 115

RESULT 8

US-09-489-039A-10294
 ; Sequence 10294, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 10294
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-10294

Query Match 100.0%; Score 31; DB 4; Length 348;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VORGR 6
 Db 165 VORGR 170

RESULT 9

US-09-252-991A-27211
 ; Sequence 27211, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 27211
 ; LENGTH: 391
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-27211

Query Match 100.0%; Score 31; DB 4; Length 391;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VORGR 6
 Db 213 VORGR 218

RESULT 10

US-09-252-991A-26099
 ; Sequence 26099, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 26099
 ; LENGTH: 863
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-26099

Query Match 100.0%; Score 31; DB 4; Length 863;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VORGR 6
 Db 9 VORGR 14

RESULT 11

US-09-252-991A-25547
 ; Sequence 25547, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25547
 ; LENGTH: 877
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25547

Query Match 100.0%; Score 31; DB 4; Length 877;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
Qy 1 VQRGR 6
Db 825 VQRGR 830

; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-750-624-3

Query Match
Best Local Similarity 96.8%; Score 30; DB 3; Length 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQRGR 6
Db 23 VQRGR 28

RESULT 14
US-09-408-020-24
; Sequence 24, Application US/09408020
; Patent No. 6632937
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCCP.002A
; CURRENT APPLICATION NUMBER: US/09/408,020
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-09-408-020-24

Query Match
Best Local Similarity 96.8%; Score 30; DB 4; Length 269;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQRGR 6
Db 55 VQRGR 60

RESULT 15
US-09-408-020-56
; Sequence 56, Application US/09408020
; Patent No. 6632937
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCCP.002A
; CURRENT APPLICATION NUMBER: US/09/408,020
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-09-408-020-56

Query Match
Best Local Similarity 96.8%; Score 30; DB 4; Length 273;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQRGR 6
```

```
Qy 1 VQRGR 6
Db 825 VQRGR 830

; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-750-624-3

Query Match
Best Local Similarity 96.8%; Score 30; DB 3; Length 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQRGR 6
Db 23 VQRGR 28

RESULT 14
US-09-408-020-24
; Sequence 24, Application US/09408020
; Patent No. 6632937
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCCP.002A
; CURRENT APPLICATION NUMBER: US/09/408,020
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-09-408-020-24

Query Match
Best Local Similarity 96.8%; Score 30; DB 4; Length 269;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQRGR 6
Db 55 VQRGR 60

RESULT 15
US-09-408-020-56
; Sequence 56, Application US/09408020
; Patent No. 6632937
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCCP.002A
; CURRENT APPLICATION NUMBER: US/09/408,020
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-09-408-020-56

Query Match
Best Local Similarity 96.8%; Score 30; DB 4; Length 273;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQRGR 6
```

Db :|||||
59 IQGGR 64

Search completed: April 15, 2004, 10:29:55
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 10:34:37 ; Search time 21 seconds
(without alignments)
27.483 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31

Sequence: 1 VQRGGR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 17 | 54.8 | 4 | 2 S47552 | ubiquitin - rat |
| 2 | 13 | 41.9 | 3 | 3 A23751 | spinal cord peptid |
| 3 | 13 | 41.9 | 5 | 2 PT0707 | T-cell receptor be |
| 4 | 13 | 41.9 | 6 | 2 A60494 | antineoplastic gly |
| 5 | 13 | 41.9 | 6 | 2 PT0514 | T-cell receptor be |
| 6 | 12 | 38.7 | 4 | 2 A53284 | T-cell receptor be |
| 7 | 12 | 38.7 | 4 | 2 B53284 | T-cell receptor be |
| 8 | 12 | 38.7 | 4 | 2 PT0706 | T-cell receptor be |
| 9 | 12 | 38.7 | 5 | 2 B61445 | Leu-enkephalin - b |
| 10 | 12 | 38.7 | 5 | 2 A61445 | Met-enkephalin - b |
| 11 | 12 | 38.7 | 5 | 2 B61168 | cocoonase (EC 3.4. |
| 12 | 12 | 38.7 | 5 | 2 PT0267 | IG heavy chain CRD |
| 13 | 12 | 38.7 | 5 | 2 C53284 | T-cell receptor be |
| 14 | 12 | 38.7 | 5 | 2 PT0669 | T-cell receptor be |
| 15 | 12 | 38.7 | 5 | 2 PT0585 | T-cell receptor be |
| 16 | 12 | 38.7 | 5 | 2 PT0717 | T-cell receptor be |
| 17 | 12 | 38.7 | 6 | 2 JU0355 | lipopeptide WS1279 |
| 18 | 12 | 38.7 | 6 | 2 PT0512 | T-cell receptor be |
| 19 | 12 | 38.7 | 6 | 2 PT0605 | T-cell receptor be |
| 20 | 12 | 38.7 | 6 | 2 PT0720 | T-cell receptor be |
| 21 | 12 | 38.7 | 6 | 2 PT0560 | T-cell receptor be |
| 22 | 12 | 38.7 | 6 | 2 PT0723 | T-cell receptor be |
| 23 | 12 | 38.7 | 6 | 2 PT0727 | T-cell receptor be |
| 24 | 12 | 38.7 | 6 | 2 PT0730 | T-cell receptor be |
| 25 | 11 | 35.5 | 4 | 1 ECXAA | antho-RFamide neur |
| 26 | 11 | 35.5 | 4 | 2 A25844 | autho-RF amide neu |
| 27 | 11 | 35.5 | 5 | 2 I40702 | primase - Citrobac |
| 28 | 11 | 35.5 | 5 | 2 S3595 | hypothetical prote |
| 29 | 11 | 35.5 | 5 | 2 PT0525 | T-cell receptor be |

30 11 35.5 5 2 PT0608 T-cell receptor be
31 11 35.5 5 2 PT0553 T-cell receptor be
32 11 35.5 5 2 PT0695 T-cell receptor be
33 11 35.5 5 2 PT0700 T-cell receptor be
34 11 35.5 6 2 S29637 Jacalin beta-II ch
35 11 35.5 6 2 I51434 H4 histone - Afric
36 11 35.5 6 2 A41946 T-cell receptor ga
37 10 32.3 5 2 PT0513 T-cell receptor be
38 10 32.3 6 2 A61411 amelestin - rat
39 10 32.3 6 2 T11779 phosphoglycerate t
40 10 32.3 6 2 A37765 hypothetical prote
41 10 32.3 6 2 PT0516 T-cell receptor be
42 9 29.0 4 2 I38888 COI intron 16 prot
43 9 29.0 5 2 JN0862 peptidyl-dipeptida
44 9 29.0 5 2 T14910 hypothetical prote
45 9 29.0 5 2 I50385 myosin light chain

ALIGNMENTS

RESULT 1

S47552

ubiquitin - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999

C;Accession: S47552

R;Hubbard, M.J.; Carne, A.

Biochim. Biophys. Acta 1200, 191-196, 1994

A;Title: Differential feeding-related regulation of ubiquitin and calbindin (9kDa) in rat

A;Reference number: S47552; MUID:94304928; PMID:8031840

A;Accession: S47552

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <HUB>

Query Match

Best Local Similarity 54.8%; Score 17; DB 2; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGG 5

Db 2 RGG 4

RESULT 2

A23751

spinal cord peptid SCP-4 - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A23751

R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tscu, K

Arch. Biochem. Biophys. 240, 178-183, 1995

A;Reference number: A23751; MUID:85250425; PMID:4015098

A;Accession: A23751

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-3 <HST>

C;Superfamily: unassigned animal peptides

Query Match

Best Local Similarity 41.9%; Score 13; DB 3; Length 3;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGG 5

Db 1 QGG 3

RESULT 3

PT0707

T-cell receptor beta chain V-D-J region (140-2H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0707; PT0705

R;Feeney, A.J. 174, 115-124, 1991

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

C;Accession: PT0707

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-5 <FEE>

A;Experimental source: strain BALB/c (clones 140-2H and 135-1DT)

C;Keywords: T-cell receptor

Query Match 41.9%; Score 13; DB 2; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGR 6

Db 3 GGQ 5

RESULT 4

A60494

Antineoplastic glycoprotein - sea hare (Dolabella auricularia) (fragment)

N;Alternate names: Dolabellin C

C;Species: Dolabella auricularia

C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 18-Jun-1993

C;Accession: A60494

R;Kisugi, J.; Kamiya, H.; Yamazaki, M.

Dev. Comp. Immunol. 13, 3-8, 1989

A;Title: Purification of dolabellin-C an antineoplastic glycoprotein in the body fluid

A;Reference number: A60494; MUID:89357188; PMID:2767307

A;Accession: A60494

A;Molecule type: protein

A;Residues: 1-6 <KIS>

C;Keywords: cytotoxicity; glycoprotein; trimer

Query Match 41.9%; Score 13; DB 2; Length 6;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RGR 6

Db 2 KSGR 5

RESULT 5

PT0514

T-cell receptor beta chain V-D-J region (100-4AC) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0514

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

C;Accession: PT0514

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEE>

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 41.9%; Score 13; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGR 6

Db 3 GGQ 5

RESULT 6

A53284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: A53284

R;Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A;Title: Evolutionarily conserved organization and sequences of germline diversity and J

A;Reference number: A53284; MUID:91342695; PMID:1678859

A;Accession: A53284

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-4 <HAR>

A;Cross-references: GB:S60737; NID:G233916; PIDN:AA19517.1; PID:G233917

A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:60739)

C;Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GG 5

Db 3 GG 4

RESULT 7

B53284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: B53284

R;Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A;Title: Evolutionarily conserved organization and sequences of germline diversity and J

A;Reference number: A53284; MUID:91342695; PMID:1678859

A;Accession: B53284

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-4 <HAR>

A;Cross-references: GB:S60737; NID:G233916; PIDN:AA19518.1; PID:G233918

A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:60738)

C;Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GG 5

Db 3 GG 4

RESULT 8

PT0706

T-cell receptor beta chain V-D-J region (135-1DU) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0706

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0706

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-4 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GG 5

Db 3 GG 4

RESULT 9

B61445
Leu-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: B61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A:Reference number: A61445; MUID:84144823; PMID:6593690
A:Accession: B61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match 38.7%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GG 5

Db 2 GG 3

RESULT 10

A61445
Met-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: A61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A:Reference number: A61445; MUID:84144823; PMID:6593690
A:Accession: A61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match 38.7%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GG 5

Db 2 GG 3

RESULT 11

B61168
cocoanase (EC 3.4.21.-) - Chinese oak silkworm (fragment)
C:Species: Antheraea pernyi (Chinese oak silkworm)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: B61168
R:Kramer, K.J.; Felsted, R.L.; Law, J.H.
J. Biol. Chem. 248, 3021-3028, 1973
A:Title: Cocoanase, V. Structural studies on an insect serine protease.
A:Reference number: A61168; MUID:73166540; PMID:4735570
A:Accession: B61168
A:Molecule type: protein
A:Residues: 1-5 <KRA>
C:Keywords: hydrolase; serine proteinase; zymogen
F,1-5/Product: cocoanase (fragment) #status experimental <MAT>

Query Match 38.7%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GG 5

Db 3 GG 4

RESULT 12

PT0267
IG heavy chain CRD3 region (clone 3-94A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0267
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0267
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 38.7%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GG 5

Db 2 GG 3

RESULT 13

C53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: C53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity and J
A:Reference number: A53284; MUID:91342695; PMID:1678859
A:Accession: C53284
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <HAR>
A:Cross-references: GB:S60737; NID:G233916; PIDN:AAE19519.1; PID:G233919
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBID:60740)
C:Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GG 5

Db 3 GG 4

RESULT 14

PT0669
T-cell receptor beta chain V-D-J region (121-3BH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0669
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0669
A>Status: translation not shown

A;Molecule type: mRNA
A;Residues: 1-5 <PEE>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GG 5
|
Db 3 GG 4

RESULT 15
PT0585
T-cell receptor beta chain V-D-J region (141-18A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0585
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; PMID:91277601; PMID:1711558
A;Accession: PT0585
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <PEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GG 5
|
Db 4 GG 5

Search completed: April 15, 2004, 10:38:23
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 10:30:51 ; Search time 12 Seconds
(without alignments)
26.035 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31

Sequence: 1 VQRGGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|--------------|---------------------|
| 1 | 11 | 35.5 | 5 | 1 UF01_MOUSE | P38639 mus musculus |
| 2 | 8 | 25.8 | 6 | 1 ACPH_RABIT | P25154 corytholagus |
| 3 | 7 | 22.6 | 5 | 1 BPP7_BOTIN | P30425 bothrops in |
| 4 | 6 | 19.4 | 3 | 1 GRWM_HUMAN | P01157 homo sapien |
| 5 | 6 | 19.4 | 4 | 1 ACHI_ACHFU | P35904 achatina fu |
| 6 | 6 | 19.4 | 4 | 1 DOWL_PSECH | P19916 pseudomonas |
| 7 | 6 | 19.4 | 4 | 1 EOSI_HUMAN | P02731 homo sapien |
| 8 | 6 | 19.4 | 4 | 1 OCP1_OCTMI | P38648 octopus min |
| 9 | 6 | 19.4 | 4 | 1 OCP3_OCTMI | P38649 octopus min |
| 10 | 6 | 19.4 | 5 | 1 ALI4_CARMA | P81817 carcinus ma |
| 11 | 6 | 19.4 | 5 | 1 PAP2_PARNA | P81864 pardachirus |
| 12 | 6 | 19.4 | 5 | 1 RE32_LITRU | P82073 litoria rub |
| 13 | 6 | 19.4 | 5 | 1 TPIS_CANFA | P54714 canis famil |
| 14 | 6 | 19.4 | 5 | 1 UXM4_CHLTR | P38005 chlamydia t |
| 15 | 6 | 19.4 | 6 | 1 CIP1_MYTED | P33736 mytilus edu |
| 16 | 6 | 19.4 | 6 | 1 CIP2_MYTED | P33737 mytilus edu |
| 17 | 6 | 19.4 | 6 | 1 FARP_MONDX | P41966 moniezia ex |
| 18 | 6 | 19.4 | 6 | 1 LOK1_LOCM1 | P41491 locusta mig |
| 19 | 5 | 16.1 | 3 | 1 THYL_PIG | P01151 sus scrofa |
| 20 | 5 | 16.1 | 4 | 1 FAR3_HIRME | P42562 hirudo medi |
| 21 | 5 | 16.1 | 4 | 1 FAR4_HIRME | P42563 hirudo medi |
| 22 | 5 | 16.1 | 4 | 1 FLRF_HIRME | P42561 hirudo medi |
| 23 | 5 | 16.1 | 4 | 1 FLRN_ATEL | P58707 anthopleura |
| 24 | 5 | 16.1 | 4 | 1 FWRP_MAGNI | P01162 macrocallis |
| 25 | 5 | 16.1 | 4 | 1 FYRI_ATEL | P58706 anthopleura |
| 26 | 5 | 16.1 | 4 | 1 TUFT_HUMAN | P01858 homo sapien |
| 27 | 5 | 16.1 | 5 | 1 FARP_ARTTR | P41853 artiposthi |
| 28 | 5 | 16.1 | 5 | 1 PRCT_PERAM | P01373 triplaneta |
| 29 | 5 | 16.1 | 5 | 1 PSK_DAUCA | P58261 daucus caro |
| 30 | 5 | 16.1 | 5 | 1 RE21_LITRU | P82071 litoria rub |
| 31 | 5 | 16.1 | 5 | 1 RE31_LITRU | P82072 litoria rub |
| 32 | 4 | 12.9 | 3 | 1 LUXE_VIBFI | P24272 vibrio fisc |
| 33 | 4 | 12.9 | 4 | 1 RM01_YEAST | P36515 saccharomyc |

| | | | | | |
|----|---|------|---|--------------|--------------------|
| 34 | 4 | 12.9 | 5 | 1 EI03_LITRU | P82099 litoria rub |
| 35 | 4 | 12.9 | 5 | 1 EI04_LITRU | P82100 litoria rub |
| 36 | 4 | 12.9 | 5 | 1 RE11_LITRU | P82070 litoria rub |
| 37 | 4 | 12.9 | 5 | 1 UC22_MAIZE | P80628 zea mays (m |
| 38 | 4 | 12.9 | 5 | 1 EI01_LITRU | P82096 litoria rub |
| 39 | 3 | 9.7 | 6 | 1 OVM_LEPDE | P42985 lepidotars |
| 40 | 3 | 9.7 | 6 | 1 DN06_CLOPA | P81351 cistridium |
| 41 | 2 | 6.5 | 4 | 1 DN05_PSECH | P19918 pseudomonas |
| 42 | 2 | 6.5 | 4 | 1 FFKA_ATEL | P58705 anthopleura |
| 43 | 2 | 6.5 | 5 | 1 TRM3_ECOLI | P13973 escherichia |
| 44 | 2 | 6.5 | 6 | 1 ASP2_LACSN | P82655 lactobacill |
| 45 | 2 | 6.5 | 6 | 1 VP19_HSVIK | P23210 herpes simp |

ALIGNMENTS

RESULT 1
UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639; 1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
TX MEDLINE=95009907; PubMed=75231108;
RA Merrick B.A., Patterson R.M., Richter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 6.6, its MW is: 19 kDa.
FT NON_TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;
Query Match 35.5%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GR 6
Db 3 GR 4

RESULT 2
ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide
hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
TX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
unblocking with N-acylaminoacyl-peptide hydrolase.";
Anal. Biochem. 199:45-50(1991).

CC -!- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal
 CC peptide bond of an N-acetylated peptide to generate an N-
 CC acetylated amino acid and a peptide with a free N-terminus. It
 CC preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.
 CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H₂O = acylamino acid
 CC + peptide.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to peptidase family S9C.
 DR PIR; A49792; A49792.
 DR INTERPRO; IPR002471; Pept_S9_AS.
 DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
 KW Hydrolase; Acetylation.
 FT MOD_RES 1 1 ACETYLATION.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;
 Query Match 25.8%; Score 8; DB 1; Length 6;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQR 3
 Db 1 MER 3
 RESULT 3
 BPP7_BOTIN STANDARD; PRT; 5 AA.
 AC P30425;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; G37196; G37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;
 Query Match 22.6%; Score 7; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QR 3
 Db 1 OK 2
 RESULT 4
 GRWM_HUMAN STANDARD; PRT; 3 AA.
 ID GRWM_HUMAN
 AC P01157;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Growth-modulating peptide.
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77162369; PubMed=858356;
 RA Schlesinger D.H., Pickart L., Thaler M.M.;
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
 RL Experientia 33:324-325(1977).
 CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
 CC growth of some cell types and to inhibit other types in vitro.
 DR GO; GO:0001558; P:regulation of cell growth; NAS.
 SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;
 Query Match 19.4%; Score 6; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 G 4
 Db 1 G 1
 RESULT 5
 ACHI_ACHFU STANDARD; PRT; 4 AA.
 ID ACHI_ACHFU
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Achatin-I.
 OS Achatina fulica (Giant African snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Sigmoethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Perussac; TISSUE=Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novalles E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Ferussac containing a D-amino acid residue.";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=Perussac; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function.";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Iwashita T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue.";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
 CC and produces a spike broadening of the identified heart excitatory
 CC neuron (PON); also enhances the amplitude and frequency of the
 CC heart beat. Has also an effect on several other muscles.
 DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.

SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 G 4
|
Db 1 G 1

RESULT 6

DCML_PSECH STANDARD; PRT; 4 AA.
ID DCML_PSECH
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTL

OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.

RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hügendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in carboxydohydrogenic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.

CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor.

CC -!- COFACTOR: Molybdenum (molybdopterin).

CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.

DR PIR; P10140; P10140.

KW Oxidoreductase; Molybdenum.

FT NON_TER 4 4

SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 G 4
|
Db 2 G 2

RESULT 7

EOSI_HUMAN STANDARD; PRT; 4 AA.
ID EOSI_HUMAN
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Eosinophilic peptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=76078412; PubMed=1060093;

RA Goetzl E.J., Austen K.F.;

RT "Purification and synthesis of eosinophilic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis."
RT Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

CC -!- MISCELLANEOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.
DR GO:0006935; P:chemotaxis; IDA.
DR GO:0006955; P:immune response; IDA.

FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
/FTID=VAR_005201.

SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 G 4
|
Db 2 G 2

RESULT 8

OCPI_OCTMI STANDARD; PRT; 4 AA.
ID OCPI_OCTMI
AC P58638;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Cardioactive peptides Ocp-1/Ocp-2.

OS Octopus minor (Octopus).

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;

OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.

OX NCBI_TaxID=89766;

RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.

RC TISSUE=Brain;

RX MEDLINE=20336815; PubMed=10876044;

RA Iwakoshi E., Hisada M., Minakata H.;

RT "Cardioactive peptides isolated from the brain of a Japanese octopus, Octopus minor".

RL Peptides 21:623-630(2000).

CC -!- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-2 is a 1000 time less active than Ocp-1.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.

CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.

KW Hormone; D-amino acid.

FT MOD_RES 2 2

SQ SEQUENCE 4 AA; 394 MW; 6AA879C310000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 G 4
|
Db 1 G 1

RESULT 9

OCPI_OCTMI STANDARD; PRT; 4 AA.
ID OCPI_OCTMI
AC P58649;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cardioactive peptides Ocp-3/Ocp-4.

OS Octopus minor (Octopus).

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;

OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.

OX NCBI_TaxID=89766;

RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.

```

RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor".
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PFM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 G 4
Db 1 G 1

RESULT 10
AL14_CARMA STANDARD; PRT; 5 AA.
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CC Eubrachyura; Portunioidea; Portunidae; Carcinus.
CX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 5 AMIDATION (POTENTIAL).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 G 4
Db 4 G 4

RESULT 11
PAP2_PARMA STANDARD; PRT; 5 AA.
ID PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81854;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

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OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus)".
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pardaxin family.
KW Toxin.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 G 4
Db 1 G 1

RESULT 12
RE32_LITRU STANDARD; PRT; 5 AA.
ID RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyllidae;
CC Pelodyadinae; Litoria.
CX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RA "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.".
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 G 4
Db 2 G 2

RESULT 13
TPIS_CANFA STANDARD; PRT; 5 AA.
ID TPIS_CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1995 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN TP11.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycero-
CC phosphate.
CC -!- PATHWAY: Plays an important role in several metabolic pathways.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the triosephosphate isomerase family.
DR HSC-2DPAGE; P54714; DOG
DR InterPro; IPR000652; Triophos_ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
KW NON_TER 1
FT NON_TER 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 G 4
Db 3 G 3

RESULT 14
UXA4 CHLTR
ID UXA4 CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 KDa.
DR Siera-2DPAGE; P38005; -.
FT NON_TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BA865AA8000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 G 4
Db 3 G 3

RESULT 15

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CIP1_MYTED
ID CIP1_MYTED STANDARD; PRT; 6 AA.
AC P3736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE=pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: Inhibitory action on contractions in several molluscan
CC muscles.
CC -!- SIMILARITY: TO MIP II.
DR PIR; A27696; A27696.
KW Hormone; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 637 MW; 72C9C6875B81000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 G 4
Db 1 G 1

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Search completed: April 15, 2004, 10:36:57
Job time : 13 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2004, 10:34:06 ; Search time 39 Seconds
(without alignments)
48.541 Million cell updates/sec

Title: US-10-625-260-8
Perfect score: 31
Sequence: 1 VQRGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 8 | 25.8 | 6 | 10 | P82181 |
| 2 | 8 | 25.8 | 6 | 10 | P82182 |
| 3 | 7 | 22.6 | 6 | 5 | P83569 |
| 4 | 6 | 19.4 | 2 | 5 | P83570 |
| 5 | 5 | 16.1 | 5 | 13 | P83308 |
| 6 | 5 | 16.1 | 6 | 10 | P82541 |
| 7 | 4 | 12.9 | 4 | 11 | Q84433 |
| 8 | 4 | 12.9 | 6 | 2 | P83533 |
| 9 | 3 | 9.7 | 4 | 5 | P83568 |
| 10 | 2 | 6.5 | 5 | 2 | P83073 |
| 11 | 2 | 6.5 | 5 | 10 | Q99007 |

ALIGNMENTS

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RESULT 1
P82181
AC P82181 PRELIMINARY; PRT; 6 AA.
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RL the 50 S subunit of an organelle ribosome (chloroplast).";
RJ J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 25.8%; Score 8; DB 10; Length 6;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VQR 3
Db 2 ISR 4

RESULT 2
P82182
AC P82182 PRELIMINARY; PRT; 6 AA.
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RL the 50 S subunit of an organelle ribosome (chloroplast).";
RJ J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
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DR InterPro; IPR002363; Ribosomal L10eub.
 DR PROSITE; PS01109; RIBOSOMAL L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
 Query Match 25.8%; Score 8; DB 10; Length 6;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VOR 3
 Db 2 ISR 4
 RESULT 3
 P83569 PRELIMINARY; PRT; 6 AA.
 ID P83569
 AC P83569
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Sperm attracting peptide SepSAP.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
 RP AMIDATION.
 RC TISSUE=Egg;
 RA Zatylny C, Marvin L, Gagnon J., Henry J.;
 RX PubMed=12207899;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 attracting peptide.";
 RL Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).
 CC -!- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE
 CC COLLISION.
 CC -!- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES DURING
 CC VITELLOGENESIS. ACCUMULATES IN THE OOCYTES BEFORE BEING SECRETED
 CC DURING FERTILIZATION. EXPRESSION CONTINUES IN THE EMBEDDED OOCYTE.
 CC ACCUMULATES IN THE EGG CAPSULE AFTER FERTILIZATION.
 CC -!- MASS SPECTROMETRY: MW=596.6; METHOD=MALDI.
 KW Amidation.
 FT MOD_RES 6
 SQ SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;
 Query Match 22.6%; Score 7; DB 5; Length 6;
 Best Local Similarity 25.0%; Pred. No. 1e+06;
 Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VOR 4
 Db 2 IDPG 5
 RESULT 4
 P83570 PRELIMINARY; PRT; 2 AA.
 ID P83570
 AC P83570
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Neuropeptide Gwa.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE=Optic lobe;
 RX PubMed=9437704;
 RA Henry J., Favrel P., Boucaud-Camou E.;

RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
 RT peptide inhibiting the motility of the mature oviduct in the
 RT cuttlefish, Sepia officinalis.";
 RL Peptides 18:1469-1474 (1997).
 CC -!- FUNCTION: REGULATORY NEUROPEPTIDE WITH MYOTROPIC ACTIVITY
 CC TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE OVIDUCT
 CC BY DECREASING TONUS, FREQUENCY AND AMPLITUDE OF CONTRACTIONS.
 CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 2
 SQ SEQUENCE 2 AA; 261 MW; 73781000000000000000 CRC64;
 Query Match 19.4%; Score 6; DB 5; Length 2;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 G 4
 Db 1 G 1
 RESULT 5
 P83308 PRELIMINARY; PRT; 5 AA.
 ID P83308
 AC P83308
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE FMRFamide-like neuropeptide (LPLRF-amide).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FMRFamide.";
 RL Nature 305:328-330 (1983).
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 5
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
 Query Match 16.1%; Score 5; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 R 3
 Db 4 R 4
 RESULT 6
 P82541 PRELIMINARY; PRT; 6 AA.
 ID P82541
 AC P82541
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=cv. ALVARO; Tissue=Leaf;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 37:28455-28465(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN P.I. S19 BETA
 FORM IS THE MINOR BASIC FORM.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR GO: GO:0009507; C:chloroplast; IEA.
 DR GO: GO:0019843; F:rRNA binding; IEA.
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
 DR InterPro: IPR002222; Ribosomal_S19.
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

 Query Match 16.1%; Score 5; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

 QY 3 R 3
 DB 2 R 2

 RESULT 7
 Q08433
 ID Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Gunn;
 RX MEDLINE=91282758; PubMed=1840486;
 RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 DR EMBL: S38636; AAB19259.1; -;
 DR GO: GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON TER 1
 SQ SEQUENCE 4 AA; 473 MW; 533732C420000000 CRC64;

 Query Match 12.9%; Score 4; DB 11; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

 QY 1 V 1
 DB 2 V 2

 RESULT 8
 P83533

ID P83533 PRELIMINARY; PRT; 6 AA.
 AC P83533;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE
 RC STRAIN=DSM 20451;
 RX PubMed=12112860;
 RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
 RT "High pressure effects step-wise altered protein expression in
 Lactobacillus sanfranciscensis.";
 RL Proteomics 2:765-774(2002).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
 CC -!- PROTEIN IS: 15 KDA.
 FT NON TER 1
 FT NON TER 6
 SQ SEQUENCE 6 AA; 590 MW; 6DDDD452D1AAC000 CRC64;

 Query Match 12.9%; Score 4; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

 QY 1 V 1
 DB 3 V 3

 RESULT 9
 P83568 PRELIMINARY; PRT; 4 AA.
 ID P83568;
 AC P83568;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Pheromone peptide ILME.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=Egg;
 RX PubMed=10944467;
 RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
 RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
 officinalis";
 RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Egg;
 RX PubMed=12207899;
 RA Zatylny C., Marvin L., Gagnon J., Henry J.;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 attracting peptide";
 RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
 CC -!- FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OOCYTE AND EGG(EC2).
 CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
 DR GO: GO:0005186; F:pheromone activity; IEA.
 KW Pheromone.
 FT NON TER 1
 SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

 Query Match 9.7%; Score 3; DB 5; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
 Matches 0; Conservative 1; Mismatches 0;

Qy 1 V 1
 Db 1 I 1

RESULT 10

P83073 PRELIMINARY; PRT; 5 AA.
 AC P83073;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 88 kDa protein (fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to Swiss-Prot.
 FT NON TER 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 6.5%; Score 2; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQ 2
 Db 1 MK 2

RESULT 11

Q99007 PRELIMINARY; PRT; 5 AA.
 AC Q99007;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Alpha amylase (fragment).
 GN AMY1 GENE.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticeae; Hordeum.
 CX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 RT acid and abscisic acid in protoplasts prepared from mature barley
 RT aleurone layers.";
 RL Plant Mol. Biol. 16:713-721(1991).
 DR EMBL; X54643; CAA38455.1; -.
 FT NON TER 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 6.5%; Score 2; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 R 3
 Db 4 K 4

Search completed: April 15, 2004, 10:37:49
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 10:30:01 ; Search time 54 Seconds
(without alignments)
31.394 Million cell updates/sec

Title: US-10-625-260-8
Perfect score: 31
Sequence: 1 VQRGGR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 59163

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 31 | 100.0 | 6 | 4 | AAB50043 Human alp |
| 2 | 23 | 74.2 | 6 | 2 | AAB50043 Peptide u |
| 3 | 23 | 74.2 | 6 | 2 | AAB50043 Peptide u |
| 4 | 22 | 71.0 | 6 | 7 | ADCI1546 Rho 110 l |
| 5 | 19 | 61.3 | 4 | 1 | ADCI1546 Rho 110 l |
| 6 | 19 | 61.3 | 6 | 2 | AAB50043 Peptide u |
| 7 | 19 | 61.3 | 6 | 6 | AAB50043 Peptide u |
| 8 | 18 | 58.1 | 5 | 1 | AAP81943 Pentapept |
| 9 | 18 | 58.1 | 5 | 2 | AAP81943 Pentapept |
| 10 | 18 | 58.1 | 6 | 3 | AAB36754 HRG-beta1 |
| 11 | 18 | 58.1 | 6 | 5 | AAB36754 HRG-beta1 |
| 12 | 18 | 58.1 | 6 | 5 | AAB36754 HRG-beta1 |
| 13 | 18 | 58.1 | 6 | 5 | AAB36754 HRG-beta1 |
| 14 | 18 | 58.1 | 6 | 5 | AAB36754 HRG-beta1 |
| 15 | 17 | 54.8 | 3 | 5 | ABG77837 Targettin |
| 16 | 17 | 54.8 | 3 | 5 | ABG77837 Targettin |
| 17 | 17 | 54.8 | 4 | 1 | AAP81943 Pentapept |
| 18 | 17 | 54.8 | 4 | 1 | AAP81943 Pentapept |
| 19 | 17 | 54.8 | 4 | 2 | AAB50043 Peptide u |
| 20 | 17 | 54.8 | 4 | 2 | AAB50043 Peptide u |
| 21 | 17 | 54.8 | 4 | 2 | AAB50043 Peptide u |
| 22 | 17 | 54.8 | 4 | 2 | AAB50043 Peptide u |
| 23 | 17 | 54.8 | 4 | 2 | AAB50043 Peptide u |
| 24 | 17 | 54.8 | 4 | 2 | AAB50043 Peptide u |
| 25 | 17 | 54.8 | 4 | 2 | AAB50043 Peptide u |

| | | | | | |
|----|----|------|---|---|--------------------|
| 26 | 17 | 54.8 | 4 | 2 | AA09567 Antimicro |
| 27 | 17 | 54.8 | 4 | 2 | AA09567 Antimicro |
| 28 | 17 | 54.8 | 4 | 3 | AA09567 Antimicro |
| 29 | 17 | 54.8 | 4 | 3 | AA09567 Antimicro |
| 30 | 17 | 54.8 | 4 | 3 | AA09567 Antimicro |
| 31 | 17 | 54.8 | 4 | 4 | AA09567 Antimicro |
| 32 | 17 | 54.8 | 4 | 4 | AA09567 Antimicro |
| 33 | 17 | 54.8 | 4 | 4 | AA09567 Antimicro |
| 34 | 17 | 54.8 | 4 | 4 | AA09567 Antimicro |
| 35 | 17 | 54.8 | 4 | 5 | ABG77837 Targettin |
| 36 | 17 | 54.8 | 4 | 5 | ABG77837 Targettin |
| 37 | 17 | 54.8 | 4 | 6 | ABG77837 Targettin |
| 38 | 17 | 54.8 | 4 | 7 | ADCI1412 Aspergill |
| 39 | 17 | 54.8 | 4 | 7 | ADCI1412 Aspergill |
| 40 | 17 | 54.8 | 5 | 1 | AAP81943 Pentapept |
| 41 | 17 | 54.8 | 5 | 1 | AAP81943 Pentapept |
| 42 | 17 | 54.8 | 5 | 1 | AAP81943 Pentapept |
| 43 | 17 | 54.8 | 5 | 2 | AAR07685 Ubiquitin |
| 44 | 17 | 54.8 | 5 | 2 | AAR07685 Ubiquitin |
| 45 | 17 | 54.8 | 5 | 2 | AAR20332 Sequence |

ALIGNMENTS

RESULT 1
AAB50043
ID AAB50043 standard; peptide; 6 AA.

XX AC AAB50043;

DT 14-MAR-2001 (first entry)

DE Human alpha1 integrin domain epitope.

XX KW Human; alpha1 integrin domain; alphanbetal function blocking antibody;
inflammatory disorder; rheumatoid arthritis; skin condition; asthma;
brucellosis; headache; antipyretic; fever; gastrointestinal;
KW vascular disease; autoimmune; respiratory distress syndrome;
XX endotoxin shock syndrome; atherosclerosis.

OS Homo sapiens.

PN WO200072881-A1.

XX PD 07-DEC-2000.

XX PF 01-JUN-2000; 2000WO-US015004.

XX PR 01-JUN-1999; 99US-0137038P.

XX PR 29-FEB-2000; 2000US-0185336P.

XX PA (BIOJ) BIOGEN INC.

XX PI De Fougereolles A, Gotwais P, Lobb R, Koteliarsky V;

XX DR WPI; 2001-061448/07.

XX PT Use of blocking monoclonal antibody capable of binding to an epitope of

XX PS VLA-1 for treating inflammatory disorders, in particular arthritis.

XX CC Claim 1; Fig 15; 60pp; English.

XX CC The present invention relates to the use of an alphanbetal function
blocking antibody capable of binding the present epitope of human alpha1
integrin domain (VLA-1). The antibody of the present invention is useful
for treating an inflammatory disorder e.g. rheumatoid arthritis, skin
related conditions such as psoriasis, eczema, burns and dermatitis,
asthma, bronchitis, menstrual cramps, tendinitis, bursitis, and the
treatment of pain and headaches, or as an antipyretic, for the treatment
of fever, gastrointestinal conditions such as inflammatory bowel
diseases, Crohn's disease, gastritis and vascular diseases, migraine
headaches, periarthritis nodosa, thyroiditis, aplastic anaemia, Hodgkin's

CC disease, rheumatic fever, type I diabetes, myasthenia gravis, multiple
 CC sclerosis, sarcoidosis, nephrotic syndrome, myocardial ischaemia,
 CC allergic rhinitis, respiratory distress syndrome, endotoxin shock
 CC syndrome and atherosclerosis
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQGRGR 6
 |||||
 Db 1 VQGRGR 6

RESULT 2
 ID AAW86183 standard; peptide; 6 AA.
 XX AAW86183;
 AC
 XX
 DT 04-MAR-1999 (first entry)
 XX
 DE Peptide used in a method for inhibiting wound contraction.
 XX
 KW Wound contraction; reduction; inhibition; tissue regeneration; scar;
 KW wound; joint motion; body deformation.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 Modified-site 1 /note= "N-terminal acetylation"
 FT
 FT
 FN US5851994-A.
 XX
 XX 22-DEC-1998.
 PD
 XX 06-JUN-1995; 95US-00473025.
 PF
 XX 28-APR-1994; 94US-00234979.
 PR
 XX (LJOL-) LA JOLLA CANCER RES FOUND.
 PA
 XX Polarek J, Schreiber R;
 PI
 XX WPI; 1999-080478/07.
 DR
 XX Inhibition of wound contraction - with peptide derivatives rich in basic
 PT amino acids.
 PT
 XX Claim 11; Col 24; 16pp; English.
 PS
 XX The invention provides methods for reduction or inhibition of wound
 CC contraction that comprises administration of a peptide having more than 3
 CC consecutive basic amino acid residues. Alternatively, the peptide
 CC contains the amino acid sequence Arg-Gly-Asp and a basic amino acid
 CC sequence, or the peptide comprises 6-30 amino acids in which at least 4
 CC out of a sequence of 6 consecutive amino acids are basic amino acids. The
 CC method is used to allow normal tissue regeneration without excessive scar
 CC formation which, in the case of large wounds, can result in loss of joint
 CC motion or major body deformation. Sequences AAW86170 to AAW86183
 CC represent specifically claimed examples of peptides that can be used in
 CC the method of the invention
 CC
 XX

Query Match 74.2%; Score 23; DB 2; Length 6;
 Best Local Similarity 80.0%; Pred. NO. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGRGR 6

Db
 RESULT 3
 AAW52128
 ID AAW52128 standard; peptide; 6 AA.
 XX
 AC AAW52128;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Human alpha-2CAR peptide.
 XX
 KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2CAR.
 XX
 OS Homo sapiens.
 XX
 FN WO200179561-A2.
 XX
 PD 25-OCT-2001.
 XX
 XX 17-APR-2001; 2001WO-US012575.
 PF
 XX 17-APR-2000; 2000US-00551744.
 PR
 XX 10-AUG-2000; 2000US-0063259.
 PR
 XX 19-OCT-2000; 2000US-00692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 XX
 DR WPI; 2001-611728/70.
 XX

Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 determining whether an individual is at increased risk of developing a
 disease associated with the corresponding receptor comprises detecting a
 polymorphic site.

Example 15-21; Page 103; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 receptor gene (I)-(III) by detecting a polymorphic site, comprising: (a)
 obtaining a sample having a polynucleotide encoding an alpha-2B, alpha-2A
 or alpha-2C or fragment or complement of; and (b) detecting a polymorphic
 site comprising nucleotide positions 901-909 of (I), a site comprising
 cytosine or guanine at position 753 of (II) or a site comprising (A)
 (ggggcgggcg) or (B) (ggggcgctag) at positions 961-972 of (III). The
 method may be used for genotyping an alpha-2B, alpha-2A or alpha-2C receptor
 gene and further used to determine whether an individual is at increased
 risk of developing a disease associated with alpha-2B, alpha-2A or alpha-2,
 comprising detecting a polymorphic site which correlate to disease
 selected from cardiovascular disease, central nervous system disease and
 combinations of these. In addition, the technique may be used to predict
 an individual's response to an alpha-2B, alpha-2A, or alpha-2C agonist (e.g.
 epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz,
 UK14304, BRL353 and combinations of these) or antagonist (e.g. yohimbine,
 prazosin, ARC 239, rauwolfine, idazoxan, tolazoline, phentolamine and
 combinations of these) by detecting the polymorphic site and correlating
 the site to a predetermined response (where the response is correlated to
 adenylyl cyclase, MAP kinase activity, phosphorylation or inositol
 phosphate levels). The present sequence is that of an alpha-2CAR peptide,
 useful to the invention

Query Match 74.2%; Score 23; DB 4; Length 6;
 Best Local Similarity 80.0%; Pred. NO. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      2 RRGGR 6
Db      :||||
        1 RRGGR 5

RESULT 4
ADCI1546
ID      ADCI1546 standard; peptide; 6 AA.
AC      ADCI1546;
XX
XX      18-DEC-2003 (first entry)
DT
DE      Rho 110 labelled leaving group peptide #2.
XX
XX      Assay; binding; target; analyte; enzyme activity.
XX
XX      Synthetic.
OS
XX      WO2003067212-A2.
FN
XX
XX      14-AUG-2003.
PD
XX
XX      21-JAN-2003; 2003WO-US001497.
PF
XX
XX      08-FEB-2002; 2002US-00071395.
PR
XX
XX      (BECI ) BECKMAN COULTER INC.
PA
XX      Bell ML;
XX
XX      WPI; 2003-689583/65.
DR
XX
XX      Assaying target analytes in a sample comprises determining the extent of
PT      binding between the target analyte and the solid support-bound ligand of
PT      the analyte useful for conducting multiplexed assays of multiple
PT      analytes.
XX
XX      Disclosure; Page 32; 48pp; English.
PS
XX
XX      The invention relates to a method for assaying target analyte(s). The
CC      steric interference is provided by a solid support (s1). The method
CC      involves assaying target analyte(s) (A) in a sample comprising providing
CC      (A) and binding ligand (1) of (A) bound to a solid support, where the
CC      support is porous, the ligand is bound within the pores of the support
CC      ability, and the pores sterically interfere with the ability of the
CC      binding ligand to bind to (A) that does not hinder the binding of all
CC      other target analyte(s) to all other binding ligand(s). The method is
CC      efficiently capable of simultaneously assaying multiple different
CC      analytes and permits each target analyte to be assayed within a dynamic
CC      assay range for that analyte. The method permits assays to be conducted
CC      within their dynamic range without a need to dilute the reactants.
CC      therefore, achieving a virtual dilution. The method permits measurement
CC      of high concentration analytes in the same reaction mixture as low
CC      concentration analytes therefore, reducing the number of separate
CC      analyses necessary to complete a full clinical menu. The measurement does
CC      not require problematic low-affinity receptors and does not significantly
CC      affect other analyses in the reaction mixture. The current sequence
CC      represents a leaving group peptide for use in a cellprobe reagent for
CC      assaying enzyme activity.
XX
XX      Sequence 6 AA;
SQ
    Query Match      71.0%; Score 22; DB 7; Length 6;
    Best Local Similarity 100.0%; Pred.No. 1.4e+06;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RRGGR 6
Db      :||||
        3 RRGGR 6

RESULT 5
AAP40375
ID      AAP40375 standard; peptide; 4 AA.
AC      AAP40375;
XX
XX      03-OCT-2002 (revised)
DT      31-JAN-1992 (first entry)
XX
XX      Sequence of N-4-nitrophenyl oligopeptide deriv.
DE
XX      Chromogenic substrate; hydrolytic enzyme; N-4-nitrophenyl oligopeptide.
XX      Synthetic.
OS
XX      Key      Location/Qualifiers
FH      Modified-site 1 /label= H-Lys(Z), Boc-Lys(Z)
FT      Modified-site 4 /label= Arg-2-methoxy-pNA, Arg-2-butoxy-pNA
FT
XX      DE3244030-A.
XX      PN
XX      30-MAY-1984.
XX      PD
XX      27-NOV-1982; 82DE-03244030.
XX      PF
XX      27-NOV-1982; 82DE-03244030.
XX      PR
XX      (BEHW ) BEHRINGERWERKE AG.
XX      PA      (BEHR ) BALDWIN EHRET HILL INC.
XX      PI      Heber H, Eberle R, Teetz V;
XX      XX
XX      WPI; 1984-141204/23.
DR
XX
XX      N-4-nitrophenyl oligopeptide derivs. - as chromogenic substrates for
PT      selective assay of protease e.g. thrombin.
PT
XX
XX      Disclosure; Table IX, Page 38; 47pp; German.
PS
XX
XX      The peptide derivs. of the invention, of which AAP40372-P40375 are
CC      examples, are useful as substrates for colorimetric detection and
CC      quantification of hydrolytic enzymes of class 3.4.21 (which split the B
CC      to 4-nitroanilide bond). They are more specific cf known substrates for
CC      certain enzymes, esp. thrombin, plasmin, kallikrein, Factor Xa, urokinase
CC      and Cl-esterase. (Updated on 03-OCT-2002 to add missing OS field.)
XX
XX      Sequence 4 AA;
SQ
    Query Match      61.3%; Score 19; DB 1; Length 4;
    Best Local Similarity 75.0%; Pred.No. 1.4e+06;
    Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RRGGR 6
Db      :||||
        1 RRGGR 4

RESULT 6
AAW56877
ID      AAW56877 standard; peptide; 6 AA.
AC      AAW56877;
XX
XX      28-JUL-1998 (first entry)
DT
XX
XX      Enzyme inhibitor peptide SEQ ID NO:78.
DE
XX      Enzyme inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active;
XX      latent; substrate subtraction phage display peptide library;
XX      identification; kinase; phosphatase; serpin.
XX

```


XX The Lys1 end group is methotrexate, and the Tyr4 end group is aminopterin
 CC -gamma-hydrazide. The conjugate is immunoreactive with and immunospecific
 CC for a target site associated with a cellular disorder, eg uterine
 CC choriocarcinoma, choriona, choriodenoma destruens, hydatiform mole, acute
 CC and subacute leukaemias, leukemic meningitis, lymphosarcoma, mycosis
 CC fungoides, lung cancers esp. squamous and small types, osteogenic sarcoma
 CC and certain tumours of the head, neck and pelvis. See also AAP71468
 XX

SQ Sequence 5 AA;
 Query Match 58.1%; Score 18; DB 1; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRGG 5
 :|||
 Db 1 KRGG 4

RESULT 9
 AAR86432
 ID AAR86432 standard; peptide; 6 AA.
 AC AAR86432;
 XX
 DT 26-JAN-1996 (first entry)
 XX
 DE Cysteine-free metal-binding peptide for in-vivo imaging.
 XX
 KW diagnostic imaging; atherosclerotic plaque; tumour; inflammation;
 KW conjugate; radiotherapy; cysteine-free; metal-binding.
 XX
 OS Synthetic.
 XX
 PN DE4337599-A1.
 XX
 PD 04-MAY-1995.
 XX
 PF 01-NOV-1993; 93DE-04337599.
 XX
 PR 01-NOV-1993; 93DE-04337599.
 XX
 PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 XX
 PI Conrad J, Dinkelborg L, Erber S, Froemmel C, Hoehne W, Kramp W;
 PI Kuettner G, Malin R, Schier H, Schneider-Mergener J, Steinbrecher R;
 XX
 DR WPI; 1995-171400/23.
 XX
 PT New cysteine-free peptide(s) and their metal ion complexes - opt.
 PT conjugated to targeting agent, useful for in vivo imaging of tumours,
 PT atherosclerotic plaque etc. and for radiotherapy.
 XX
 PS Claim 6; Page 18; 25pp; German.
 XX
 CC New peptides of formula R1-X-R2 are provided, together with their
 CC conjugates with peptides, proteins, biomolecules and macromolecules,
 CC their complexes with metal ions and their water-soluble salts; where X is
 CC a chain of up to 20 alpha, beta, and/or gamma amino acid residues,
 CC including at least one Met, Arg, Lys or Asn but no Cys; R1 is H or a
 CC hydrocarbyl or acyl group, or a bond to a conjugate; and R2 is OH,
 CC hydrocarboxy or an optionally substituted amine group (forming an
 CC amide), or a bond to a conjugate. The peptides are useful when complexed
 CC to a metal (e.g. 99m-Tc) for in-vivo diagnostic imaging and therapy of
 CC tumours, organs and foci of inflammation. Conjugates of the peptides can
 CC be targetted to specific tissues. A particular application is imaging of
 CC atherosclerotic plaque. Metal is bound with good in-vivo stability;
 CC unbound material is rapidly cleared; and there is no allergic reaction.
 CC Since the peptides are free of Cys, they can be prepared simply and
 CC rapidly and can be presented in the form of a kit for radio-
 CC pharmaceutical production. The present sequence is a specific example of
 CC the new peptides

XX SQ Sequence 6 AA;
 Query Match 58.1%; Score 18; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRGG 5
 :|||
 Db 1 KRGG 4

RESULT 10
 AAB36754
 ID AAB36754 standard; peptide; 6 AA.
 AC AAB36754;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE HRG-beta1 library B variant 6.
 XX
 KW Heregulin; ErbB receptor; transplantation; cancer;
 KW nervous system disease; musculature; epithelium.
 XX
 OS Unidentified.
 XX
 PN US6136558-A.
 XX
 PD 24-OCT-2000.
 XX
 PF 09-FEB-1998; 98US-00020880.
 XX
 PR 10-FEB-1997; 97US-0037581P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jones JT, Fairbrother WJ, Ballinger MD, Wells JA, Sliwkowski MX;
 XX
 DR WPI; 2000-678767/66.
 XX
 PT New variants of heregulin, useful e.g. for treating cancer, comprises
 PT specific amino acid alterations that increase affinity for ErbB
 PT receptors.
 XX
 PS Example 3; Col 71; 58pp; English.
 XX
 CC The present invention relates to variants of heregulin that can bind to
 CC an ErbB receptor and include a portion of the 175-230 region of native
 CC human heregulin-beta1. The variants may be used to promote ex vivo
 CC survival, proliferation and differentiation of cells, particularly when
 CC intended for transplantation. They may also be used to treat a wide range
 CC of cancers and diseases of the nervous system, musculature and epithelium
 XX

SQ Sequence 6 AA;
 Query Match 58.1%; Score 18; DB 3; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VORGG 5
 :|||
 Db 2 VOREG 6

RESULT 11
 AAU84117
 ID AAU84117 standard; peptide; 6 AA.
 AC AAU84117;
 XX
 DT 08-MAY-2002 (first entry)
 XX

DE Zinc finger recognition helix peptide sequence #17.
 XX Interaction trap assay; protein-protein interaction; TRS; DBD;
 KW protein-DNA interaction; or protein-RNA interaction; DNA binding domain;
 XW transcriptional regulatory sequence; zinc finger domain.
 OS Synthetic.
 XX
 XX WO200188197-A2.
 XX
 XX PD 22-NOV-2001.
 XX
 XX PF 16-MAY-2001; 2001WO-US015718.
 XX
 XX PR 16-MAY-2000; 2000US-0204509P.
 XX
 XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 XX PI Young JK, Miller J, Pabo CO;
 XX
 XX WPI; 2002-083007/11.
 XX
 XX Interaction trap assays to detect protein-protein, protein-DNA, protein-
 PT RNA interaction by using reporter genes which upon expression confer
 PT growth advantage on host cell or result in detectable fluorescent signal.
 XX
 XX Example 1; Fig 3A; 196pp; English.
 XX
 XX The present invention relates to methods for interaction trap assays for
 CC detecting protein-protein, protein-DNA, or protein-RNA interactions. The
 CC method involves selecting an interacting pair of test polypeptides, and
 CC using a population of prokaryotic cells which contain a reporter gene
 CC operably linked to a transcriptional regulatory sequence (TRS) which
 CC includes binding sites (DNA binding domain (DBD) recognition elements)
 CC for DBD, and a chimeric gene encoding a fusion protein that includes the
 CC DBD and test polypeptide. The methods of the invention are useful for
 CC selecting test agents that modulate protein-protein, protein-DNA, or
 CC protein-RNA interactions. The test agent can be a peptide, nucleic acid,
 CC carbohydrate, natural product extract library or small organic molecule.
 CC The methods are also useful for selecting test agents that differentially
 CC modulate the interaction of a polypeptide with at least two different
 CC test polypeptides or selecting a test agent that differentially modulates
 CC the interaction of the polypeptide with at least two different DNA
 CC sequences. AAU84101-AAU84192 represent zinc finger recognition sequences
 CC that can bind to DNA
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 58.1%; Score 18; DB 5; Length 6;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QRGGR 6
 ||| :
 Db 1 QRGNK 5
 RESULT 12
 AAU84113
 ID AAU84113 standard; peptide; 6 AA.
 XX
 XX AC AAU84113;
 XX
 XX DT 08-MAY-2002 (first entry)
 XX
 XX DE Zinc finger recognition helix peptide sequence #13.
 XX
 XX Interaction trap assay; protein-protein interaction; TRS; DBD;
 KW protein-DNA interaction; or protein-RNA interaction; DNA binding domain;
 XW transcriptional regulatory sequence; zinc finger domain.
 XX
 XX OS Synthetic.
 XX

PN WO200188197-A2.
 XX
 XX PD 22-NOV-2001.
 XX
 XX PF 16-MAY-2001; 2001WO-US015718.
 XX
 XX PR 16-MAY-2000; 2000US-0204509P.
 XX
 XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 XX PI Young JK, Miller J, Pabo CO;
 XX
 XX WPI; 2002-083007/11.
 XX
 XX Interaction trap assays to detect protein-protein, protein-DNA, protein-
 PT RNA interaction by using reporter genes which upon expression confer
 PT growth advantage on host cell or result in detectable fluorescent signal.
 XX
 XX Example 1; Fig 3A; 196pp; English.
 XX
 XX The present invention relates to methods for interaction trap assays for
 CC detecting protein-protein, protein-DNA, or protein-RNA interactions. The
 CC method involves selecting an interacting pair of test polypeptides, and
 CC using a population of prokaryotic cells which contain a reporter gene
 CC operably linked to a transcriptional regulatory sequence (TRS) which
 CC includes binding sites (DNA binding domain (DBD) recognition elements)
 CC for DBD, and a chimeric gene encoding a fusion protein that includes the
 CC DBD and test polypeptide. The methods of the invention are useful for
 CC selecting test agents that modulate protein-protein, protein-DNA, or
 CC protein-RNA interactions. The test agent can be a peptide, nucleic acid,
 CC carbohydrate, natural product extract library or small organic molecule.
 CC The methods are also useful for selecting test agents that differentially
 CC modulate the interaction of a polypeptide with at least two different
 CC test polypeptides or selecting a test agent that differentially modulates
 CC the interaction of the polypeptide with at least two different DNA
 CC sequences. AAU84101-AAU84192 represent zinc finger recognition sequences
 CC that can bind to DNA
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 58.1%; Score 18; DB 5; Length 6;
 Best Local Similarity 60.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QRGGR 6
 ||| :
 Db 1 QRGNK 5
 RESULT 13
 AAU84112
 ID AAU84112 standard; peptide; 6 AA.
 XX
 XX AC AAU84112;
 XX
 XX DT 08-MAY-2002 (first entry)
 XX
 XX DE Zinc finger recognition helix peptide sequence #12.
 XX
 XX Interaction trap assay; protein-protein interaction; TRS; DBD;
 KW protein-DNA interaction; or protein-RNA interaction; DNA binding domain;
 XW transcriptional regulatory sequence; zinc finger domain.
 XX
 XX OS Synthetic.
 XX
 XX PN WO200188197-A2.
 XX
 XX PD 22-NOV-2001.
 XX
 XX PF 16-MAY-2001; 2001WO-US015718.
 XX
 XX PR 16-MAY-2000; 2000US-0204509P.
 XX
 XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 XX PI Young JK, Miller J, Pabo CO;
 XX
 XX WPI; 2002-083007/11.
 XX
 XX Interaction trap assays to detect protein-protein, protein-DNA, protein-
 PT RNA interaction by using reporter genes which upon expression confer
 PT growth advantage on host cell or result in detectable fluorescent signal.
 XX
 XX Example 1; Fig 3A; 196pp; English.
 XX
 XX The present invention relates to methods for interaction trap assays for
 CC detecting protein-protein, protein-DNA, or protein-RNA interactions. The
 CC method involves selecting an interacting pair of test polypeptides, and
 CC using a population of prokaryotic cells which contain a reporter gene
 CC operably linked to a transcriptional regulatory sequence (TRS) which
 CC includes binding sites (DNA binding domain (DBD) recognition elements)
 CC for DBD, and a chimeric gene encoding a fusion protein that includes the
 CC DBD and test polypeptide. The methods of the invention are useful for
 CC selecting test agents that modulate protein-protein, protein-DNA, or
 CC protein-RNA interactions. The test agent can be a peptide, nucleic acid,
 CC carbohydrate, natural product extract library or small organic molecule.
 CC The methods are also useful for selecting test agents that differentially
 CC modulate the interaction of a polypeptide with at least two different
 CC test polypeptides or selecting a test agent that differentially modulates
 CC the interaction of the polypeptide with at least two different DNA
 CC sequences. AAU84101-AAU84192 represent zinc finger recognition sequences
 CC that can bind to DNA
 XX
 XX Sequence 6 AA;
 SQ

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Young JK, Miller J, Pabo CO;

XX WPI; 2002-083007/11.

XX Interaction trap assays to detect protein-protein, protein-DNA, protein-RNA interaction by using reporter genes which upon expression confer

PT growth advantage on host cell or result in detectable fluorescent signal.

XX Example 1; Fig 3A; 196pp; English.

XX The present invention relates to methods for interaction trap assays for
CC detecting protein-protein, protein-DNA, or protein-RNA interactions. The
CC method involves selecting an interacting pair of test polypeptides, and
CC using a population of prokaryotic cells which contain a reporter gene
CC operably linked to a transcriptional regulatory sequence (TRS) which
CC includes binding sites (DNA binding domain (DBD) recognition elements)
CC for DBD, and a chimeric gene encoding a fusion protein that includes the
CC DBD and test polypeptide. The methods of the invention are useful for
CC selecting test agents that modulate protein-protein, protein-DNA, or
CC protein-RNA interactions. The test agent can be a peptide, nucleic acid,
CC carbohydrate, natural product extract library or small organic molecule.
CC The methods are also useful for selecting test agents that differentially
CC modulate the interaction of a polypeptide with at least two different
CC test polypeptides or selecting a test agent that differentially modulates
CC the interaction of the polypeptide with at least two different DNA
CC sequences. AAU84101-AAU84192 represent zinc finger recognition sequences
CC that can bind to DNA

XX Sequence 6 AA;

Query Match 58.1%; Score 18; DB 5; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRGR 6

DB 1 QRGK 5

RESULT 14

AAU84118
ID AAU84118 standard; peptide; 6 AA.

AC AAU84118;

DT 08-MAY-2002 (first entry)

DE Zinc finger recognition helix peptide sequence #18.

KW Interaction trap assay; protein-protein interaction; TRS; DBD;
KW protein-DNA interaction; or protein-RNA interaction; DNA binding domain;
KW transcriptional regulatory sequence; zinc finger domain.

XX Synthetic.

XX WO200188197-A2.

XX 22-NOV-2001.

XX 16-MAY-2001; 2001WO-US015718.

XX 16-MAY-2000; 2000US-0204509P.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Young JK, Miller J, Pabo CO;

XX WPI; 2002-083007/11.

XX Interaction trap assays to detect protein-protein, protein-DNA, protein-RNA interaction by using reporter genes which upon expression confer

PT growth advantage on host cell or result in detectable fluorescent signal.

XX Example 1; Fig 3A; 196pp; English.

XX The present invention relates to methods for interaction trap assays for
CC detecting protein-protein, protein-DNA, or protein-RNA interactions. The
CC method involves selecting an interacting pair of test polypeptides, and
CC using a population of prokaryotic cells which contain a reporter gene
CC operably linked to a transcriptional regulatory sequence (TRS) which
CC includes binding sites (DNA binding domain (DBD) recognition elements)
CC for DBD, and a chimeric gene encoding a fusion protein that includes the
CC DBD and test polypeptide. The methods of the invention are useful for
CC selecting test agents that modulate protein-protein, protein-DNA, or
CC protein-RNA interactions. The test agent can be a peptide, nucleic acid,
CC carbohydrate, natural product extract library or small organic molecule.
CC The methods are also useful for selecting test agents that differentially
CC modulate the interaction of a polypeptide with at least two different
CC test polypeptides or selecting a test agent that differentially modulates
CC the interaction of the polypeptide with at least two different DNA
CC sequences. AAU84101-AAU84192 represent zinc finger recognition sequences
CC that can bind to DNA

XX Sequence 6 AA;

Query Match 58.1%; Score 18; DB 5; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRGR 6

DB 1 QRGK 5

RESULT 15

ABG77837
ID ABG77837 standard; peptide; 3 AA.

AC ABG77837;

DT 05-NOV-2002 (first entry)

DE Targeting peptide selective for human organ, tissue or cell type #370.

XX Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;
XX immunomodulator; antibacterial; antiviral; gene therapy; cancer;
XX arthritis; diabetes; inflammatory disease; atherosclerosis;
XX autoimmune disease; bacterial infection; viral infection;
XX cardiovascular disease; degenerative disease.

XX Homo sapiens.

XX WO200220723-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028044.

XX 08-SEP-2000; 2000US-0231266P.

XX 17-JAN-2001; 2001US-00765101.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-599247/64.

XX New targeting peptides identified by phage display, useful for treating a
XX disease state, e.g. cancer, diabetes, inflammatory disease,
XX atherosclerosis, autoimmune disease, bacterial or viral infection or
XX cardiovascular disease.

XX Example 3; Page 83; 269pp; English.

CC The invention describes an isolated peptide of 100 amino acids or less in
 CC size. The peptide is useful for treating a disease state, e.g. cancer,
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune
 CC disease, bacterial infection, viral infection, cardiovascular disease or
 CC degenerative disease. This sequence represents a human targeting peptide
 CC selective for human organs, tissues or cell types
 XX
 SQ Sequence 3 AA;

Query Match 54.8%; Score 17; DB 5; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGG 5
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 Db 1 RGG 3

Search completed: April 15, 2004, 10:36:34
 Job time : 58 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2004, 10:37:52 ; Search time 41 Seconds
(without alignments)
40.342 Million cell updates/sec

Title: US-10-625-260-8

Perfect score: 31

Sequence: 1 VQGRGR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 25053

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 31 | 100.0 | 6 | 9 | US-09-996-738-8 |
| 2 | 31 | 100.0 | 6 | 9 | US-09-996-738-9 |
| 3 | 31 | 100.0 | 6 | 12 | US-10-625-260-8 |
| 4 | 31 | 100.0 | 6 | 14 | US-10-061-658-8 |
| 5 | 23 | 74.2 | 6 | 14 | US-10-001-073-51 |
| 6 | 21 | 67.7 | 6 | 15 | US-10-137-867-58 |
| 7 | 19 | 61.3 | 6 | 12 | US-10-464-302-59 |
| 8 | 19 | 61.3 | 6 | 12 | US-10-464-302-68 |
| 9 | 19 | 61.3 | 6 | 14 | US-10-348-232-78 |
| 10 | 18 | 58.1 | 6 | 9 | US-09-990-762-30 |
| 11 | 18 | 58.1 | 6 | 9 | US-09-990-762-31 |
| 12 | 18 | 58.1 | 6 | 9 | US-09-990-762-42 |
| 13 | 18 | 58.1 | 6 | 10 | US-09-858-852A-30 |
| 14 | 18 | 58.1 | 6 | 10 | US-09-858-852A-31 |
| 15 | 18 | 58.1 | 6 | 10 | US-09-858-852A-42 |

| | | | | | | |
|----|----|------|---|----|--------------------|-------------------|
| 16 | 18 | 58.1 | 6 | 12 | US-10-464-302-55 | Sequence 55, Appl |
| 17 | 18 | 58.1 | 6 | 12 | US-10-464-302-64 | Sequence 64, Appl |
| 18 | 18 | 58.1 | 6 | 14 | US-10-083-747A-54 | Sequence 54, Appl |
| 19 | 17 | 54.8 | 4 | 9 | US-09-779-233-31 | Sequence 31, Appl |
| 20 | 17 | 54.8 | 4 | 9 | US-09-834-765-756 | Sequence 756, App |
| 21 | 17 | 54.8 | 4 | 9 | US-09-925-796-7 | Sequence 7, Appli |
| 22 | 17 | 54.8 | 4 | 9 | US-09-941-450-7 | Sequence 7, Appli |
| 23 | 17 | 54.8 | 4 | 9 | US-09-947-387-55 | Sequence 5, Appli |
| 24 | 17 | 54.8 | 4 | 9 | US-09-947-387-56 | Sequence 55, Appl |
| 25 | 17 | 54.8 | 4 | 9 | US-09-947-387-57 | Sequence 56, Appl |
| 26 | 17 | 54.8 | 4 | 9 | US-09-947-387-57 | Sequence 57, Appl |
| 27 | 17 | 54.8 | 4 | 9 | US-09-942-087A-7 | Sequence 7, Appli |
| 28 | 17 | 54.8 | 4 | 9 | US-09-942-090-7 | Sequence 7, Appli |
| 29 | 17 | 54.8 | 4 | 10 | US-09-897-844-7 | Sequence 7, Appli |
| 30 | 17 | 54.8 | 4 | 14 | US-10-028-075B-152 | Sequence 152, App |
| 31 | 17 | 54.8 | 4 | 14 | US-10-029-206A-152 | Sequence 152, App |
| 32 | 17 | 54.8 | 4 | 14 | US-10-245-415B-7 | Sequence 7, Appli |
| 33 | 17 | 54.8 | 4 | 14 | US-10-412-105-31 | Sequence 31, Appl |
| 34 | 17 | 54.8 | 4 | 14 | US-10-412-105-31 | Sequence 31, Appl |
| 35 | 17 | 54.8 | 4 | 15 | US-10-138-375-55 | Sequence 55, Appl |
| 36 | 17 | 54.8 | 4 | 15 | US-10-138-375-56 | Sequence 56, Appl |
| 37 | 17 | 54.8 | 4 | 15 | US-10-138-375-57 | Sequence 57, Appl |
| 38 | 17 | 54.8 | 5 | 9 | US-09-967-003-3 | Sequence 3, Appli |
| 39 | 17 | 54.8 | 5 | 9 | US-09-977-831-17 | Sequence 17, Appl |
| 40 | 17 | 54.8 | 5 | 9 | US-09-947-387-96 | Sequence 96, Appl |
| 41 | 17 | 54.8 | 5 | 9 | US-09-947-387-97 | Sequence 97, Appl |
| 42 | 17 | 54.8 | 5 | 9 | US-09-947-387-101 | Sequence 101, App |
| 43 | 17 | 54.8 | 5 | 9 | US-09-947-387-102 | Sequence 102, App |
| 44 | 17 | 54.8 | 5 | 9 | US-09-947-387-135 | Sequence 135, App |
| 45 | 17 | 54.8 | 5 | 9 | US-09-947-387-136 | Sequence 136, App |

ALIGNMENTS

RESULT 1
US-09-996-738-8
; Sequence 8, Application US/09996738
; Patent No. US20020146417A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: De Fougereolles, Antonin
; APPLICANT: Gotwals, Philip
; APPLICANT: Lobb, Roy
; APPLICANT: Koreliansky, Victor
; TITLE OF INVENTION: Method for the Treatment of Inflammatory
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: A076PCT
; CURRENT APPLICATION NUMBER: US/09/996,738
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/185336
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/137038
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo Sapiens

US-09-996-738-8
Query Match 100.0%; Score 31; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQGRGR 6
|||
Db 1 VQGRGR 6

RESULT 2
US-09-996-738-9


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; Sequence 9, Application US/09996738
; Patent No. US20020146417A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: De Fougereolles, Antonin
; APPLICANT: Gotwals, Philip
; APPLICANT: Lobb, Roy
; APPLICANT: Koteliarsky, Victor
; TITLE OF INVENTION: Method for the Treatment of Inflammatory
; FILE REFERENCE: A076PCT
; CURRENT APPLICATION NUMBER: US/09/996,738
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/185336
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/137038
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-996-738-9

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Query Match      100.0%; Score 31; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VQRGGR 6
Db      1 VQRGGR 6

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RESULT 3
US-10-625-260-8
; Sequence 8, Application US/10625260
; Publication No. US20040037827A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Gotwals, Philip
; APPLICANT: Koteliarsky, Victor
; TITLE OF INVENTION: Method for the Treatment of Fibrosis
; FILE REFERENCE: A073US
; CURRENT APPLICATION NUMBER: US/10/625,260
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: 60/137,214
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/130,847
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-625-260-8

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Query Match      100.0%; Score 31; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VQRGGR 6
Db      1 VQRGGR 6

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RESULT 4
US-10-061-658-8
; Sequence 8, Application US/10061658
; Publication No. US20020182213A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.

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; APPLICANT: Gotwals, Philip
; APPLICANT: Koteliarsky, Victor
; TITLE OF INVENTION: Method for the Treatment of Fibrosis
; FILE REFERENCE: A073US
; CURRENT APPLICATION NUMBER: US/10/061,658
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/137,214
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/130,847
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-061-658-8

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Best Local Similarity 100.0%; Pred. No. 1e+06;
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QY      1 VQRGGR 6
Db      1 VQRGGR 6

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RESULT 5
US-10-001-073-51
; Sequence 51, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-51

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Best Local Similarity 80.0%; Pred. No. 1e+06;
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QY      2 QRGGR 6
Db      1 RRGGR 5

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RESULT 6
US-10-137-867-58
; Sequence 58, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

```

APPLICANT: Tamas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C146
CURRENT APPLICATION NUMBER: US/10/137,867
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 58
LENGTH: 486
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-867-58

Query Match 67.7%; Score 21; DB 15; Length 6;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VQGRG 6
Db 1 IERSGR 6

RESULT 7
US-10-464-302-59
Sequence 59, Application US/10464302
Publication No. US2004003775A1
GENERAL INFORMATION:
APPLICANT: SIAHAAN, TERUNA J.
APPLICANT: YUSUF-MAKAGIANSAR, HELENA
APPLICANT: ANDERSON, MEAGAN
APPLICANT: XU, RONG CHRISTINE
TITLE OF INVENTION: LEUKOCYTE INTERNALIZED PEPTIDE-DRUG CONJUGATES
FILE REFERENCE: 23838-08028
CURRENT APPLICATION NUMBER: US/10/464,302
CURRENT FILING DATE: 2003-06-17
Prior Application Number: 09/629,719
Prior Filing Date: 2000-08-01
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 59
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-464-302-59

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Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGRG 6
Db 2 RGKG 5

RESULT 8
US-10-464-302-68
Sequence 68, Application US/10464302
Publication No. US2004003775A1
GENERAL INFORMATION:
APPLICANT: SIAHAAN, TERUNA J.
APPLICANT: YUSUF-MAKAGIANSAR, HELENA
APPLICANT: ANDERSON, MEAGAN
APPLICANT: XU, RONG CHRISTINE
TITLE OF INVENTION: LEUKOCYTE INTERNALIZED PEPTIDE-DRUG CONJUGATES
FILE REFERENCE: 23838-08028
CURRENT APPLICATION NUMBER: US/10/464,302

CURRENT FILING DATE: 2003-06-17
Prior Application Number: 09/629,719
Prior Filing Date: 2000-08-01
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 68
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-464-302-68

Query Match 61.3%; Score 19; DB 12; Length 6;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGRG 6
Db 2 RGKG 5

RESULT 9
US-10-348-232-78
Sequence 78, Application US/10348232
Publication No. US20030186329A1
GENERAL INFORMATION:
APPLICANT: Madison, Edwin L.
APPLICANT: Ke, Song-Hua
TITLE OF INVENTION: USE OF SUBSTRATE SUBTRACTION LIBRARIES TO DISTINGUISH
FILE REFERENCE: TSRI 543.1C1
CURRENT APPLICATION NUMBER: US/10/348,232
CURRENT FILING DATE: 2003-01-21
Prior Application Number: US 09/202,265
Prior Filing Date: 1999-03-22
Prior Application Number: PCT/US97/09760
Prior Filing Date: 1997-06-10
Prior Application Number: US 60/019,495
Prior Filing Date: 1996-06-10
NUMBER OF SEQ ID NOS: 244
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 78
LENGTH: 6
TYPE: PRT
ORGANISM: Homo sapiens
US-10-348-232-78

Query Match 61.3%; Score 19; DB 14; Length 6;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGRG 6
Db 1 RGKG 4

RESULT 10
US-09-990-762-30
Sequence 30, Application US/09990762
Patent No. US20020119498A1
GENERAL INFORMATION:
APPLICANT: JOUNG, J. KEITH
APPLICANT: MILLER, JEFFREY
APPLICANT: PABO, CARL O.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
FILE REFERENCE: MTV-030.02 (20021-30021)
CURRENT APPLICATION NUMBER: US/09/990,762
CURRENT FILING DATE: 2001-11-14
Prior Application Number: 09/858,852
Prior Filing Date: 2001-05-16
Prior Application Number: 60/204,509

; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-30

Query Match 58.1%; Score 18; DB 9; Length 6;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRGR 6
||| :
Db 1 QRGNK 5

RESULT 11

US-09-990-762-31
; Sequence 31, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-31

Query Match 58.1%; Score 18; DB 9; Length 6;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRGR 6
||| :
Db 1 QRGNK 5

RESULT 12

US-09-990-762-42
; Sequence 42, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16

; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-42

Query Match 58.1%; Score 18; DB 9; Length 6;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRGR 6
||| :
Db 1 QRGNK 5

RESULT 13

US-09-858-852A-30
; Sequence 30, Application US/09858852A
; Publication No. US20030044787A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.01 (20021-3001)
; CURRENT APPLICATION NUMBER: US/09/858,852A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-858-852A-30

Query Match 58.1%; Score 18; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRGR 6
||| :
Db 1 QRGNK 5

RESULT 14

US-09-858-852A-31
; Sequence 31, Application US/09858852A
; Publication No. US20030044787A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.01 (20021-3001)
; CURRENT APPLICATION NUMBER: US/09/858,852A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-858-852A-31
Query Match      58.1%; Score 18; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2 ORGGR 6
      ||| :
Db      1 QRGKX 5

```

```

RESULT 15
US-09-858-852A-42
; Sequence 42, Application US/09858852A
; Publication No. US2003004787A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.01 (20021-3001)
; CURRENT APPLICATION NUMBER: US/09/858,852A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-858-852A-42

```

```

Query Match      58.1%; Score 18; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      2 ORGGR 6
      ||| :
Db      1 QRGKX 5

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Search completed: April 15, 2004, 10:43:27
Job time : 41 secs

| Result No. | Score | Query Match | Length | DB | ID | Description | |
|------------|-------|-------------|--------|----|--------------------|-------------------|--|
| | | | | | | | |
| 1 | 31 | 100.0 | 6 | 4 | US-10-061-658-8 | Sequence 8, Appl | |
| 2 | 23 | 74.2 | 6 | 2 | US-08-473-025-18 | Sequence 18, Appl | |
| 3 | 19 | 61.3 | 5 | 4 | US-09-717-364A-36 | Sequence 36, Appl | |
| 4 | 18 | 58.1 | 6 | 3 | US-09-020-880-56 | Sequence 54, Appl | |
| 5 | 18 | 58.1 | 6 | 3 | US-08-635-928-9 | Sequence 9, Appl | |
| 6 | 18 | 58.1 | 6 | 4 | US-09-101-544-54 | Sequence 54, Appl | |
| 7 | 17 | 54.8 | 3 | 4 | US-09-360-237-12 | Sequence 12, Appl | |
| 8 | 17 | 54.8 | 4 | 1 | US-08-100-744-6 | Sequence 6, Appl | |
| 9 | 17 | 54.8 | 4 | 1 | US-08-284-784-6 | Sequence 6, Appl | |
| 10 | 17 | 54.8 | 4 | 2 | US-08-854-811-6 | Sequence 6, Appl | |
| 11 | 17 | 54.8 | 4 | 2 | US-08-685-589A-14 | Sequence 14, Appl | |
| 12 | 17 | 54.8 | 4 | 2 | US-08-685-589A-23 | Sequence 23, Appl | |
| 13 | 17 | 54.8 | 4 | 2 | US-08-350-260A-306 | Sequence 306, App | |
| 14 | 17 | 54.8 | 4 | 2 | US-08-350-260A-398 | Sequence 398, App | |
| 15 | 17 | 54.8 | 4 | 2 | US-09-017-205-71 | Sequence 71, Appl | |
| 16 | 17 | 54.8 | 4 | 3 | US-09-357-952-55 | Sequence 55, Appl | |
| 17 | 17 | 54.8 | 4 | 3 | US-09-357-952-56 | Sequence 56, Appl | |
| 18 | 17 | 54.8 | 4 | 3 | US-09-357-952-57 | Sequence 57, Appl | |
| 19 | 17 | 54.8 | 4 | 4 | US-09-521-650-55 | Sequence 55, Appl | |
| 20 | 17 | 54.8 | 4 | 4 | US-09-521-650-56 | Sequence 56, Appl | |
| 21 | 17 | 54.8 | 4 | 4 | US-09-521-650-57 | Sequence 57, Appl | |
| 22 | 17 | 54.8 | 4 | 4 | US-09-168-888-55 | Sequence 55, Appl | |
| 23 | 17 | 54.8 | 4 | 4 | US-09-168-888-56 | Sequence 56, Appl | |
| 24 | 17 | 54.8 | 4 | 4 | US-09-168-888-57 | Sequence 57, Appl | |
| 25 | 17 | 54.8 | 4 | 4 | US-09-240-179-51 | Sequence 51, Appl | |
| 26 | 17 | 54.8 | 4 | 4 | US-09-104-337A-306 | Sequence 306, App | |
| 27 | 17 | 54.8 | 4 | 4 | US-09-104-337A-398 | Sequence 398, App | |

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,025
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,979
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1597
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /note= "The amino acid, Arg, is acetylated at the N-terminal."
US-08-473-025-18

Query Match 74.2%; Score 23; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QRRGR 6
DB 2 RRGR 6

RESULT 3
US-09-717-364A-36
Sequence 36, Application US/09717364A
Patent No. 6663872

GENERAL INFORMATION:
APPLICANT: Pitkovski, Jacob
APPLICANT: Muellem, Margalit
APPLICANT: Koren, Ziv Reil
APPLICANT: Krispel, Simcha
APPLICANT: Shmueli, Esther
APPLICANT: Peretz, Yifat
APPLICANT: Gutter, Bezael
APPLICANT: Gallili, Gilad
APPLICANT: Michael, Amnon
APPLICANT: Goldberg, Doron
TITLE OF INVENTION: HEMORRHAGIC ENTERITIS VIRUS DNA SEQUENCES, PROTEINS ENCODED THEREOF
FILE REFERENCE: 1567/63655
CURRENT APPLICATION NUMBER: US/09/717,364A
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: IL124567
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: PCT/IL9900268
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 5
TYPE: PRT
ORGANISM: hemorrhagic enteritis virus
US-09-717-364A-36

Query Match 61.3%; Score 19; DB 4; Length 5;

Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGR 6
DB 2 RGR 5

RESULT 4
US-09-020-880-54
Sequence 54, Application US/09020880A
Patent No. 6136558

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Jones, Jennifer T.
APPLICANT: Fairbrother, Wayne J.
APPLICANT: Sliwowski, Mark X.
APPLICANT: Wells, James A.
TITLE OF INVENTION: HERGULIN VARIANTS
FILE REFERENCE: 14918-720CON1
CURRENT APPLICATION NUMBER: US/09/020,880A
CURRENT FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: US 60/037,581
EARLIER FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 6
TYPE: PRT
ORGANISM: No. 6136558 relevant (recombinant)
US-09-020-880-54

Query Match 58.1%; Score 18; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VORGG 5
DB 2 VORGG 6

RESULT 5
US-08-635-928-9
Sequence 9, Application US/08635928
Patent No. 6291639

GENERAL INFORMATION:
APPLICANT: CONRAD, JURGEN
APPLICANT: DINKELBORG, LUDGER
APPLICANT: ERBER, SEBASTIAN
APPLICANT: FROMMEL, CORNEIUS
APPLICANT: HOHNE, WOLFGANG
APPLICANT: KRAMP, WOLFGANG
APPLICANT: KUTTNER, GABRIELE
APPLICANT: MALIN, REINHARD
APPLICANT: SCHIER, HANS MARTIN
APPLICANT: SCHNIDER-MERGENER, JENS
TITLE OF INVENTION: METAL-BINDING CYSTEIN-FREE PEPTIDES FOR DIAGNOSTIC AND THERAPEUTICAL PURPOSES, METHODS FOR THEIR
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLIESLER, DUBB, MEYER & LOVEJOY LLP
STREET: Four Embarcadero Center, Suite 400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS

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; SOFTWARE: WordPerfect 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,928
; FILING DATE: 09/20/96
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DE94/01302
; FILING DATE: 10/27/94
; APPLICATION NUMBER: P4337599.5
; FILING DATE: 11/01/93
; ATTORNEY/AGENT INFORMATION:
; NAME: Molano, Michael A.
; REGISTRATION NUMBER: 39,777
; REFERENCE/DOCKET NUMBER: WBUT2010(WO/US)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-362-3800
; TELEFAX: 415-362-2928
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-635-928-9

```

```

Query Match 58.1%; Score 18; DB 3; Length 6;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 QRG 5
Db 1 RRG 4

```

```

RESULT 6
US-09-101-544-54
; Sequence 54, Application US/09101544
; Patent No. 6387638
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 14918-720CON2
; CURRENT APPLICATION NUMBER: US/09/101,544
; CURRENT FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: US 09/020,880
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/037,581
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 6
; TYPE: PRT
; ORGANISM: No. 6387638 relevant (recombinant)
; US-09-101-544-54

```

```

Query Match 58.1%; Score 18; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 VORG 5
Db 2 VORG 6

```

```

RESULT 7
US-09-360-237-12
; Sequence 12, Application US/09360237
; Patent No. 6323662
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAWSON, ROBERT B.
; APPLICANT: SAKAI, JUO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
; US-09-360-237-12

```

```

Query Match 54.8%; Score 17; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 4 GGR 6
Db 1 GGR 3

```

```

RESULT 8
US-08-100-744-6
; Sequence 6, Application US/08100744
; Patent No. 5563046
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, DESMOND
; APPLICANT: ZHANG, SUNNY
; APPLICANT: OLSEN, PAMELA
; APPLICANT: OLSEN, DAVID
; APPLICANT: CARRILLO, PEDRO A.
; TITLE OF INVENTION: POLYPEPTIDE FUSIONS TO
; INTERLEUKIN-1-LIKE POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,744
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: 22095-20275.00

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-100-744-6

Query Match 54.8%; Score 17; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGG 5
DB 2 RGG 4

RESULT 9
US-08-284-784-6
Sequence 6, Application US/08284784
Patent No. 5629172
GENERAL INFORMATION:
APPLICANT: MASCARENHAS, DESMOND
APPLICANT: ZHANG, YANG
APPLICANT: OLSON, PAMELA S.
APPLICANT: OLSEN, DAVID R.
APPLICANT: CARILLO, PEDRO A.
TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER SEQUENCES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,784
FILING DATE: 02-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 22095-20275.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-284-784-6

Query Match 54.8%; Score 17; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGG 5
DB 2 RGG 4

RESULT 10
US-08-854-811-6
Sequence 6, Application US/08854811
Patent No. 5914254
GENERAL INFORMATION:
APPLICANT: Mascarenhas, Desmond
APPLICANT: Zhang, Yang
APPLICANT: Olson, Pamela S.
APPLICANT: Olsen, David R.
APPLICANT: Cohen, Pedro A.
TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,811
FILING DATE: 12-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/284,784
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/100,744
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Buffinger, Nicholas S
REGISTRATION NUMBER: 39,124
REFERENCE/DOCKET NUMBER: 22095-20275.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-854-811-6

Query Match 54.8%; Score 17; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGG 5
DB 2 RGG 4

RESULT 11
US-08-685-589A-14
Sequence 14, Application US/08685589A
Patent No. 5916872
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222


```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: No. 5916872 Relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
; US-08-685-589A-14

Query Match 54.8%; Score 17; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGR 6
Db 2 GGR 4

RESULT 12
US-08-685-589A-23
; Sequence 23, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: No. 5916872 Relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
; US-08-685-589A-23

Query Match 54.8%; Score 17; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGG 5
Db 1 RGG 3

RESULT 13
US-08-350-260A-306
; Sequence 306, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9

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;/ FILING DATE: 24-MAR-1992
;/ PRIOR APPLICATION DATA: PCT/GB91/01134
;/ APPLICATION NUMBER: GB 9206318.9
;/ FILING DATE: 10-JUL-1991
;/ PRIOR APPLICATION DATA: PCT/GB92/00883
;/ FILING DATE: 15-MAY-1992
;/ PRIOR APPLICATION DATA: PCT/GB93/00605
;/ FILING DATE: 24-MAR-1993
;/ PRIOR APPLICATION DATA: US 08/150,002
;/ FILING DATE: 31-MAR-1994
;/ PRIOR APPLICATION DATA: US 08/307,619
;/ FILING DATE: 16-SEP-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Clough, David W
;/ REGISTRATION NUMBER: 36,107
;/ REFERENCE/DOCKET NUMBER: 28111/32372
;/ TELEPHONE: 312-474-6300
;/ INFORMATION FOR SEQ ID NO: 306:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 4 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-350-260A-306

Query Match 54.8%; Score 17; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 4 GGR 6
Db 1 GGR 3

RESULT 14
US-08-350-260A-398
; Sequence 398, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4

;/ FILING DATE: 15-MAY-1991
;/ PRIOR APPLICATION DATA: PCT/GB91/01134
;/ APPLICATION NUMBER: GB 9206318.9
;/ FILING DATE: 24-MAR-1992
;/ PRIOR APPLICATION DATA: PCT/GB91/01134
;/ APPLICATION NUMBER: PCT/GB92/00883
;/ FILING DATE: 15-MAY-1992
;/ PRIOR APPLICATION DATA: PCT/GB93/00605
;/ FILING DATE: 24-MAR-1993
;/ PRIOR APPLICATION DATA: US 08/150,002
;/ FILING DATE: 31-MAR-1994
;/ PRIOR APPLICATION DATA: US 08/307,619
;/ FILING DATE: 16-SEP-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Clough, David W
;/ REGISTRATION NUMBER: 36,107
;/ REFERENCE/DOCKET NUMBER: 28111/32372
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 312-474-6300
;/ INFORMATION FOR SEQ ID NO: 398:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 4 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-350-260A-398

Query Match 54.8%; Score 17; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGR 6
Db 1 GGR 3

RESULT 15
US-09-017-205-71
; Sequence 71, Application US/09017205
; Patent No. 5965357
; GENERAL INFORMATION:
; APPLICANT: Marsden, Howard S
; TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
; TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 5965357th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,205
; FILING DATE: 02-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide from HSV-2 glycoprotein G
; FRAGMENT TYPE: internal
US-09-017-205-71

Query Match 54.8%; Score 17; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGG 5
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DB 1 RGG 3

Search completed: April 15, 2004, 10:42:05
Job time : 23 secs